

<110> Hoorn, Gert
Menke, Annette

<130> C=0293us/JH/ml

<14C>

<141>

 $\langle 160 \rangle$ 4-

<170> PatentIn Ver. 2.1

<210> 1

<211> 12

<212> R:::

<213> Influenza A virus

<400> 1

ccugcuuz:zg cu

12

<210> 2

<211> 12

<212> RNE

<213> Influenza B virus

 $\langle 220 \rangle$

<221> misc feature

$$\langle 222 \rangle \quad (1 \quad \bar{1} \quad 2)$$

<223> n = any nucleotide

<400> 2

nnygcucczg cu

12

 $\langle 210 \rangle$ 3

<211> 12

<212> R.N.E.

<213> Influenza C virus

 $\langle 400 \rangle$ 3°

ccugcuucag cu

12

<210> 4

<211> 12

<212> R::三

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Modified influenza A 3'-sequence

<400\ 4

ccugauuu -a cu

12

<210> 5

 $\langle 211 \rangle \quad 12$

<212> RME

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified influenza A 3'-sequence

cc:iguuuuua cu

12

<211> 12

<212> RNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified influenza A 3'-sequence

cc:ggguucuc cu

12

$\langle 2\bar{1}1 \rangle$ 13

<212> RNA

<213> Influenza A virus

aguagaaca agg

13

<211> 13

<212> RNA

<213> Influenza B virus

<221> misc feature

$\langle 222 \rangle$ (12) . (13)

<223> n = any nucleotide

aguagwaaca rnn

13

$\langle 211 \rangle$ 13

<212> RNA

<213> Influenza C virus

agcaguagca agr

13

 $\langle 211 \rangle$ 13 $\langle 2-2 \rangle \ni NA$

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified influenza A 5'-sequence

agaagaauca agg

13

<210> 11
 <211> 11
 <212> RNA
 <213> Influenza A virus

<220>
 <221> misc_feature
 <222> 14)..(16)
 <223> n = any nucleotide

<400> 11
 aguagaaaca aggnnnuuuu u

21

<210> 12
 <211> 21
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 influenza A 5'-sequence (pHL1920)

<220>
 <221> misc_feature
 <222> (14)..(16)
 <223> n = any nucleotide

<400> 12
 agaagaauca aggnnnuuuu u

21

<210> 13
 <211> 21
 <212> RNA
 <213> Influenza B virus

<220>
 <221> misc_feature
 <222> (12)..(16)
 <223> n = any nucleotide

<400> 13
 aguagwaaca rnnnnnnuuuu u

21

<210> 14
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 Influenza C 5'-sequence

<400> 14
 aguaguaaca agrguuuuu

19

<210> 15
 <211> 17
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 Influenza A 3'-sequence (pHL1102)

20250722 14:00:00

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n = any nucleotide

<400> 15
 nnnccuguuu uuacu

15

<210> 16
 <211> 15
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 influenza A 3'-sequence (pHL1104 and pHL1920)

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n = any nucleotide

<400> 16
 nnnccuguuu cuacu

15

<210> 17
 <211> 15
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 influenza A 3'-sequence (pHL1948)

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n = any nucleotide

<400> 17
 nnnccugguu cuccu

15

<210> 18
 <211> 15
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 influenza B 3' sequence

<220>
 <221> misc_feature
 <222> (1)..(5)
 <223> n = any nucleotide

<400> 18
 nnnnnyguuu cuacu

15

<210> 19
 <211> 14
 <212> RNA

20250220 14:44:00

gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa Glu	cca Pro	agt Ser 80	gga Gly	tat Tyr	gca Ala	caa Gln	aca Thr 85	gac Asp	tgc Cys	gtc Val	ctg Leu	gaa Glu 90	gca Ala	atg Met	gct Ala	469
ttc Phe	ctt Leu 95	gaa Glu	gaa Glu	tcc Ser	cat His	cca Pro 100	gga Gly	atc Ile	ttt Phe	gaa Glu	aac Asn 105	tcg Ser	tgt Cys	ctt Leu	gag Glu	517
acg Thr 110	atg Met	gaa Glu	gtt Val	gtt Val	caa Gln 115	caa Gln	aca Thr	aga Arg	gtg Val	gac Asp 120	aaa Lys	ctg Leu	acc Thr	caa Gln	ggc Gly 125	565
cgt Arg	cag Gln	act Thr	tat Tyr	gat Asp 130	tgg Trp	act Thr	ttg Leu	aat Asn 135	aga Arg	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	act Thr	613
gca Ala	tta Leu	gca Ala	aac Asn 145	act Thr	ata Ile	gag Glu	gtc Val	ttt Phe 150	aga Arg	tcg Ser	aat Asn	ggt Gly	cta Leu 155	aca Thr	gct Ala	661
aat Asn	gaa Glu	tca Ser 160	ggg Gly	agg Arg	ctc Leu	ata Ile	gat Asp 165	ttc Phe	ctc Leu	aag Lys	gat Asp 170	gtg Val	atg Met	gaa Glu	tca Ser	709
atg Met	gat Asp 175	aag Lys	gag Glu	gaa Glu	atg Met	gag Glu 180	ata Ile	aca Thr	aca Thr	cat His	ttc Phe 185	caa Gln	cga Arg	aag Lys	aga Arg	757
aga Arg 190	gta Val	aga Arg	gac Asp	aac Asn	atg Met 195	acc Thr	aag Lys	aaa Lys	atg Met	gtc Val 200	aca Thr	caa Gln	aga Arg	aca Thr	ata Ile 205	805
ggg Gly	aag Lys	aaa Lys	aag Lys	cag Gln 210	aga Arg	ctt Leu	aac Asn	aaa Lys	agg Arg 215	agc Ser	tac Tyr	cta Leu	ata Ile	agg Arg 220	gct Ala	853
cta Leu	aca Thr	ttg Leu	aac Asn 225	aca Thr	atg Met	acg Thr	aaa Lys	gat Asp 230	gca Ala	gaa Glu	aga Arg	ggt Gly	aaa Lys 235	ctg Leu	aag Lys	901
aga Arg	aga Arg	gca Ala 240	att Ile	gca Ala	aca Thr	cca Pro	ggg Gly 245	atg Met	cag Gln	atc Ile	aga Arg	ggg Gly 250	ttt Phe	gtg Val	tac Tyr	949
ttt Phe	gtt Val 255	gag Glu	aca Thr	ctg Leu	gcg Ala	aga Arg 260	agc Ser	att Ile	tgc Cys	gag Glu	aag Lys 265	ctt Leu	gaa Glu	cag Gln	tct Ser	997
ggg Gly 270	cta Leu	cca Pro	gtt Val	gga Gly	ggg Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gct Ala 280	aaa Lys	ttg Leu	gca Ala	aat Asn	gtc Val 285	1045
gtg Val	agg Arg	aag Lys	atg Met	atg Met	acg Thr 290	aac Asn	tca Ser	caa Gln	gac Asp 295	act Thr	gag Glu	ctc Leu	tct Ser	ttc Phe	aca Thr 300	1093
atc Ile	acc Thr	gga Gly	gac Asp 305	aat Asn	acc Thr	aaa Lys	tgg Trp	aat Asn 310	gag Glu	aac Asn	caa Gln	aac Asn	ccc Pro 315	cga Arg	atg Met	1141
ttc Phe	ctg Leu	gca Ala 320	atg Met	ata Ile	aca Thr	tac Tyr	atc Ile 325	aca Thr	aga Arg	aac Asn	caa Gln	cct Pro 330	gag Glu	tgg Trp	ttt Phe	1189
aga Arg	aat Asn 335	gtc Val	ttg Leu	agc Ser	atc Ile	gcg Ala 340	ccg Pro	ata Ile	atg Met	ttt Phe	tcg Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg 365
 350 355 360

aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 380
 370 375

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile 395
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 410
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 425
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 445
 430 435 440

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 460
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met 475
 465 470 475

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr 490
 480 485 490

agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu 505
 495 500 505

ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 525
 510 515 520 525

gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro 540
 530 535 540

gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr 555
 545 550 555

aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser 570
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu 585
 575 580 585

ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 605
 590 595 600 605

10073370000

atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att 2101
 Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile
 625 630 635

gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys
 640 645 650

agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag 2197
 Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

agc agc tca tac aga aga cca gtt gga att tcc agt atg gtg gag gcc 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715

atg gtg tct agg gcc cgg att gat gca cga att gac ttc gag tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

att gaa gag ctc aga cgg cag aaa tagtgaatgt agcttgctcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611
 cacggacacc tgtcccaaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671
 tctggtcaac ccaggacac acgcggggagc agcgcggggc cggggacgcc ctcccggccg 2731
 cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggcccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 ccccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091
 ctataaagat accaggcggt tccccctgga agctccctcg tcgcctctcc tgttccgacc 3151
 ctgccgctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcgggt taggtcgttc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331

200020-222222

aaccgcggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
gcgaggtatg taggcggtgc tacagagttc ttgaagtggg ggccctaacta cggctacact 3451
agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtgggtttttt tgtttgcaag 3571
cagcagatta cgcgagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
tctgacgctc agtggaaacga aaactcacgt taagggattt tggatcatgag attatcaaaa 3691
aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataat ctaaagtata 3751
tatgagtaaa cttggtctga cagttaccaa tgcttaata gtaggcacc tatctcagcg 3811
atctgtctat ttcggtcacc catagttgcc tgactccccg tcgtgtagat aactacgata 3871
cgggaggggt taccatctgg cccagtgct gcaatgatac cgcgagacc acgctcaccg 3931
gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgag aagtggccct 3991
gcaactttat ccgcctccat ccagtctatt aattggtgcc gggaagctag agtaagtagt 4051
tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
tcgtcgtttg gtatggcttc attcagctcc ggttcccaac gatcaaggcg agttacatga 4171
tccccatgt tgtgcaaaaa agcgggttagc tccttcggtc ctccgatcgt tgtcagaagt 4231
aagttggccg cagtgttacc actcatggtt atggcagcac tgcataattc tottactgtc 4291
atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
tagtgatgc gccgaccgag ttgctcttgc ccggcgtaaa caccgggataa taccgcgcca 4411
catagcagaa ctttaaaagt gtcctcatt ggaaaacgtt ctccggggcg aaaactctca 4471
aggatcttac cgctgttgag atccagttcg atgtaacca ctctgcacc caactgatct 4531
tcagcatctt ttactttcac cagcgtttct ggtgagcaa aaacaggaag gcaaaatgcc 4591
gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cttttttcaa 4651
tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
tagaaaaata aacaaaagag ttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771
ctgcttaatt tgatgcctgg cagtttatgg cggcgctcct gcccgccacc ctccgggccg 4831
ttgcttcgca acgttcaaat ccgtcccg cggtttgtc ctactcagga gagcgttcac 4891
cgacaaaca cagataaaac gaaaggcca gtctttcgac tgagcctttc gttttatttg 4951
atgcttgga gttccctact ctgcgatgg gagacccac actaccatcg gcgctacggc 5011
gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgccaaggc 5071
aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaaatc 5131
tctctcatcc gccaaaacag ccaagctagc ggccgatc 5169

<210> 23

<211> 757

<212> PRT

<223> Description of Artificial Sequence: FPV-Br.-PB1

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asp Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly
			340					345					350		
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Leu	Arg	Thr	Gln	Ile
		355					360					365			
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Glu	Pro
	370					375					380				
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Ile	Ile	Asp	Gly	Thr
385					390					395					400
Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	Met	Leu	Ser
				405					410					415	
Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	Gly	Gln	Lys	Arg	Tyr	Thr
			420					425					430		
Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	Asp	Phe	Ala
		435					440					445			
Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	Gly	Val	Asp
	450					455					460				
Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Val	Gly	Ile	Asn	Met	Ser	Lys	Lys
465					470					475					480
Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	Phe	Glu	Phe	Thr	Ser	Phe	Phe
				485					490					495	
Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	Met	Glu	Leu	Pro	Ser	Phe
			500					505					510		
Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	Met	Ser	Ile	Gly	Val	Thr
		515					520					525			
Val	Ile	Lys	Asn	Asn	Met	Ile	Asn	Asn	Asp	Leu	Gly	Pro	Ala	Thr	Ala
	530					535					540				
Gln	Met	Ala	Leu	Gln	Leu	Phe	Ile	Lys	Asp	Tyr	Arg	Tyr	Thr	Tyr	Arg
545					550					555					560
Cys	His	Arg	Gly	Asp	Thr	Gln	Ile	Gln	Thr	Arg	Arg	Ser	Phe	Glu	Leu
				565					570					575	
Lys	Lys	Leu	Trp	Glu	Gln	Thr	Arg	Ser	Lys	Ala	Gly	Leu	Leu	Val	Ser
			580					585					590		
Asp	Gly	Gly	Pro	Asn	Leu	Tyr	Asn	Ile	Arg	Asn	Leu	His	Ile	Pro	Glu
		595					600					605			
Val	Cys	Leu	Lys	Trp	Glu	Leu	Met	Asp	Glu	Asp	Tyr	Gln	Gly	Arg	Leu
	610					615					620				
Cys	Asn	Pro	Met	Asn	Pro	Phe	Val	Ser	His	Lys	Glu	Ile	Glu	Ser	Val
625					630					635					640
Asn	Asn	Ala	Ala	Val	Met	Pro	Ala	His	Gly	Pro	Ala	Lys	Ser	Met	Glu
				645					650					655	
Tyr	Asp	Ala	Val	Ala	Thr	Thr	His	Ser	Trp	Ile	Pro	Lys	Arg	Asn	Arg
			660					665					670		
Ser	Ile	Leu	Asn	Thr	Ser	Gln	Arg	Gly	Ile	Leu	Glu	Asp	Glu	Gln	Met
		675					680					685			

<400>	24															
ccccaaaaaaaa	aaaaaaaaaa	aagag	tccag	agtgg	ccccg	ccgct	ccgcg	ccg	ggggggg	60						
ggggggggggg	ggacactttc	ggacat	ctg	tcgac	ctcca	gcac	cgggg	aaaaaaaaa	120							
acaaagtgtc	gcccggagta	ctggtc	gacc	tccga	agttg	ggggg	gagcg	aaagc	aggca	180						
aaccatttga	atg	gat	gtc	aat	ccg	act	tta	ctt	ttc	tta	aaa	gtg	cca	229		
	Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro			
	1				5					10						
gca	caa	aat	gct	ata	agc	aca	act	ttc	cct	tat	act	gga	gac	cct	cct	277
Ala	Gln	Asn	Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	
	15					20					25					
tac	agc	cat	ggg	aca	gga	aca	gga	tac	acc	atg	gat	act	gtc	aac	agg	325
Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	
	30				35					40					45	
aca	cat	cag	tac	tca	gaa	agg	gga	aga	tgg	aca	aca	aac	acc	gaa	act	373
Thr	His	Gln	Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	
				50					55					60		
gga	gca	ccg	caa	ctc	aac	ccg	att	gat	ggg	cca	ctg	cca	gaa	gac	aat	421
Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	
			65					70					75			
gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	
		80					85					90				
ttc	ctt	gag	gaa	tcc	cat	cct	ggt	atc	ttt	gag	acc	tcg	tgt	ctt	gaa	517
Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	
	95					100					105					
acg	atg	gag	gtt	gtt	cag	caa	aca	cga	gtg	gac	aag	ctg	aca	caa	ggc	565
Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	
110					115					120					125	

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
 350 355 360 365

act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
 Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile
 385 390 395

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat 1525
 Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg 1621
 Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met
 465 470 475

agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu
 495 500 505

ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
 510 515 520 525

gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
 Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
 625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
 640 645 650

20250727 080000

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2197
 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665
 aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685
 gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700
 agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715
 atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730
 agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745
 att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755
 atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctcccccg ggccgggagg tcgcgtcacc gaccacgcc cgggcccagg cgacgcgcga 2611
 cacggacacc tgtccccaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671
 tctggtcaac ccaggacac acgcgggagc agcgccgggc cggggacgcc ctccgggccg 2731
 cccgtgccac acgcaggggg cgggcccggtg tctccagagc gggagccgga agcattttcg 2791
 gccggccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggcgcac gcgcgtcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa ccgacagga 3091
 ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttcogacc 3151
 ctgcgctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgt gtaggtatct cagttcggtg taggtcgttc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331
 aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcggtgc tacagagttc ttgaagtggg ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtgggttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
 tctgacgctc agtggaacga aaactcacgt taagggattt tggatcatgag attatcaaaa 3691

20220727 14:00:00

aggatcttca cctagatcct tttaaattaa aatgaagtt ttaaataaat ctaaagtata 3751
 tatgagtaaa cttggtctga cagttaccaa tgcttaatca gtgaggcacc tatctcagcg 3811
 atctgtctat ttctgttcac catagtggcc tgactccccg tcgtgtagat aactacgata 3871
 cgggaggggt taccatctgg cccagtggt gcaatgatac cgcgagaccc acgtccaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgagc aagtggctct 3991
 gcaactttat ccgcctccat ccagtcctatt aattgttgcc gggaaagctag agtaagtagt 4051
 tcgccagtra atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc ggttcccaac gatcaaggcg agttacatga 4171
 tccccatgt tgtgcaaaaa agcgggttagc tccttcgggc ctccgacgtg tgcagaagt 4231
 aagttggccg cagtgttacc actcatgggt atggcagcac tgcataattc tcttactgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgatgc gccgaccgag ttgctcttgc ccggcgctcaa cacgggataa taccgcgcca 4411
 catagcagaa ctttaaaagt gtcctcatt ggaaaacgtt cttcggggcg aaaactctca 4471
 aggatcttac cgctgttgag atccagttcg atgtaacca ctcgtgcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct ggggtgagcaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cttttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
 tagaaaaata aacaaaagag tttgtagaaa ccaaaaaagg ccatccgtca ggatggcctt 4771
 ctgcttaatt tgatgcctgg cagtttatgg cgggcgtcct gcccgccacc ctccggggcg 4831
 ttgcttcgca acgttcaaat ccgctcccg cggatttgct ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
 atgcctggca gttccctact ctgcctggg gagacccacc actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgtactg ccgccaggca 5071
 aattctgtt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ccgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctagc gcccgatc 5169

<210> 25

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: WSN-PB1

<400> 25

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
 1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
 20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
	50					55					60				
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser
65					70					75					80
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu
				85					90					95	
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu
			100				105						110		
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
		115					120					125			
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala
	130					135					140				
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser
145					150					155					160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys
				165					170					175	
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
			180					185					190		
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
		195					200					205			
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
	210					215					220				
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
225					230					235					240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
				245					250					255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro
			260					265					270		
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys
		275					280					285			
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly
	290					295					300				
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala
305					310					315					320
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val
				325					330					335	
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly
			340					345					350		
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	Thr	Gln	Ile
		355					360					365			
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Asp	Ser
	370					375					380				
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ile	Asp	Gly	Thr
385					390					395					400

Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
405 410 415

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
420 425 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
435 440 445

Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
565 570 575

Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

20220220 14:00:00

Leu Arg Arg Gln Lys
755

```
<210> 26
<211> 5169
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: pHL3102

```
<220>
<221> CDS
<222> (191)..(2461)
```

<400>	26																
cccaaaaaaaaa	aaaaa	aaagagtccag	agtggccccg	ccgttccgcg	ccgggggggg	60											
gggggggggg	ggacactttc	ggacatctgg	tcgacctcca	gcacggggg	aaaaaaaaa	120											
acaaagtgtc	gcccggagta	ctggctgacc	tccgaagttg	ggggggagcg	aaagcaggca	180											
aaccatttga	atg	gat	gtc	aat	ccg	act	tta	ctt	ttc	tta	aaa	gtg	cca		229		
	Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro				
	1				5					10							
gca	caa	aat	gct	ata	agc	aca	act	ttc	cct	tat	act	gga	gac	cct	cct	277	
Ala	Gln	Asn	Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro		
	15					20					25						
tac	agc	cat	ggg	aca	gga	aca	gga	tac	acc	atg	gat	act	gtc	aac	agg	325	
Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg		
	30				35				40						45		
aca	cat	cag	tac	tca	gaa	agg	gga	aga	tgg	aca	aca	aac	acc	gaa	act	373	
Thr	His	Gln	Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr		
				50					55					60			
gga	gca	ccg	caa	ctc	aac	ccg	att	gat	ggg	cca	ctg	cca	gaa	gac	aat	421	
Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn		
			65					70					75				
gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469	
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala		
		80					85					90					
ttc	ctt	gag	gaa	tcc	cat	cct	ggt	atc	ttt	gag	acc	tcg	tgt	ctt	gaa	517	
Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu		
	95					100					105						
acg	atg	gag	gtt	gtt	cag	caa	aca	cga	gtg	gac	aag	ctg	aca	caa	ggc	565	
Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly		
	110				115				120						125		
cga	cag	acc	tat	gac	tgg	act	cta	aat	agg	aac	cag	cct	gct	gca	aca	613	
Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr		
				130					135					140			
gca	ttg	gcc	aac	aca	ata	gaa	gtg	ttc	aga	tca	aat	ggc	ctc	acg	gcc	661	
Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala		
			145					150					155				
aat	gaa	tct	gga	agg	ctc	ata	gac	ttc	ctt	aag	gat	gta	atg	gag	tca	709	
Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser		
		160					165					170					

10222000

atg Met	aac Asn 175	aaa Lys	gaa Glu	gaa Glu	atg Met	gag Glu 180	atc Ile	aca Thr	act Thr	cat His	ttt Phe 185	cag Gln	aga Arg	aag Lys	aga Arg	757
cga Arg 190	gtg Val	aga Arg	gac Asp	aat Asn	atg Met 195	act Thr	aag Lys	aaa Lys	atg Met	gtg Val 200	aca Thr	cag Gln	aga Arg	aca Thr	ata Ile 205	805
ggt Gly	aaa Lys	agg Arg	aag Lys	cag Gln 210	aga Arg	ttg Leu	aac Asn	aaa Lys	agg Arg 215	agt Ser	tat Tyr	cta Leu	att Ile	agg Arg 220	gca Ala	853
tta Leu	acc Thr	ctg Leu	aac Asn 225	aca Thr	atg Met	acc Thr	aaa Lys	gat Asp 230	gct Ala	gag Glu	aga Arg	ggg Gly	aag Lys 235	cta Leu	aaa Lys	901
cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg	ggg Gly 250	ttt Phe	gta Val	tac Tyr	949
ttt Phe	ggt Val 255	gag Glu	aca Thr	cta Leu	gca Ala	agg Arg 260	agt Ser	ata Ile	tgt Cys	gag Glu	aaa Lys 265	ctt Leu	gaa Glu	caa Gln	tca Ser	997
gga Gly 270	ttg Leu	cca Pro	gtt Val	gga Gly	ggc Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gca Ala 280	aag Lys	ttg Leu	gca Ala	aat Asn	gtt Val 285	1045
gta Val	agg Arg	aag Lys	atg Met	atg Met 290	acc Thr	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
atc Ile	act Thr	gga Gly	gat Asp 305	aac Asn	acc Thr	aaa Lys	tgg Trp	aac Asn 310	gaa Glu	aat Asn	cag Gln	aac Asn	cct Pro 315	cgg Arg	atg Met	1141
ttt Phe	ttg Leu	gcc Ala 320	atg Met	atc Ile	aca Thr	tat Tyr	ata Ile 325	acc Thr	aga Arg	aat Asn	cag Gln	ccc Pro 330	gaa Glu	tgg Trp	ttc Phe	1189
aga Arg	aat Asn 335	gtt Val	cta Leu	agt Ser	att Ile	gct Ala 340	cca Pro	ata Ile	atg Met	ttc Phe	tca Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237
aga Arg 350	ctg Leu	gga Gly	aag Lys	ggg Gly	tac Tyr 355	atg Met	ttt Phe	gag Glu	agc Ser	aag Lys 360	agt Ser	atg Met	aaa Lys	att Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	cct Pro	gca Ala 370	gaa Glu	atg Met	cta Leu	gca Ala 375	agc Ser	atc Ile	gat Asp	ttg Leu	aaa Lys	tac Tyr 380	ttc Phe	1333
aat Asn	gat Asp	tca Ser	act Thr 385	aga Arg	aag Lys	aag Lys	att Ile	gaa Glu 390	aaa Lys	atc Ile	cgg Arg	ccg Pro	ctc Leu 395	tta Leu	ata Ile	1381
gat Asp	ggg Gly	act Thr 400	gca Ala	tca Ser	ttg Leu	agc Ser	cct Pro 405	gga Gly	atg Met	atg Met	atg Met	ggc Gly 410	atg Met	ttc Phe	aat Asn	1429
atg Met	tta Leu 415	agt Ser	act Thr	gta Val	tta Leu	ggc Gly 420	gtc Val	tcc Ser	atc Ile	ctg Leu	aat Asn 425	ctt Leu	gga Gly	caa Gln	aag Lys	1477
aga Arg 430	cac His	acc Thr	aag Lys	act Thr	act Thr 435	tac Tyr	tgg Trp	tgg Trp	gat Asp	ggg Gly 440	ctt Leu	caa Gln	tct Ser	tct Ser	gat Asp 445	1525

gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc	1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg	1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca	1669
Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt gga gta tca gga att aat gaa tgc gct gat atg agc att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat	1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr	
545 550 555	
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	
ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg	1957
Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu	
575 580 585	
ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac	2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His	
590 595 600 605	
atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag	2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln	
610 615 620	
gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att	2101
Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile	
625 630 635	
gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa	2149
Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys	
640 645 650	
agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag	2197
Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys	
655 660 665	
aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat	2245
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp	
670 675 680 685	
gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct	2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro	
690 695 700	

10073377.020802

agc	agc	tca	tac	aga	aga	cca	gtt	gga	att	tcc	agt	atg	gtg	gag	gcc	2341
Ser	Ser	Ser	Tyr	Arg	Arg	Pro	Val	Gly	Ile	Ser	Ser	Met	Val	Glu	Ala	
			705					710					715			
atg	gtg	tct	agg	gcc	cgg	att	gat	gca	cga	att	gac	ttc	gag	tct	gga	2389
Met	Val	Ser	Arg	Ala	Arg	Ile	Asp	Ala	Arg	Ile	Asp	Phe	Glu	Ser	Gly	
			720				725					730				
agg	att	aag	aag	gaa	gag	ttt	gct	gag	atc	atg	aag	atc	tgt	tcc	acc	2437
Arg	Ile	Lys	Lys	Glu	Glu	Phe	Ala	Glu	Ile	Met	Lys	Ile	Cys	Ser	Thr	
			735			740					745					
att	gaa	gag	ctc	aga	cgg	caa	aaa	tagtgaattt	agctt	gtcct	tcatg	aaaaa				2491
Ile	Glu	Glu	Leu	Arg	Arg	Gln	Lys									
					750	755										
atgcctt	gtt	tct	actaata	acccg	ggcgc	ccaaa	atg	gactc	gggagc	gaa	agatata					2551
cctcccc	cgg	ggccg	gggagg	tcgcgt	cacc	gaccac	gcgc	cgggcc	cagg	cgacgc	gcga					2611
cacggac	acc	tgtcccc	aaa	aacgc	ccacca	tcgcag	ccac	acacgg	gagcg	cccggg	ggccc					2671
tctggt	caac	cccagg	acac	acgcgg	gagc	agcgcc	gggc	cgggg	acgcc	ctccc	ggccg					2731
cccgtg	ccac	acgcagg	ggg	ccggccc	gtg	tctcc	agagc	gggag	cgcga	agcatt	tttcg					2791
gccggccc	ct	cctacg	accg	ggacac	acga	gggacc	gaag	gccggc	cagg	cgcgac	ctct					2851
cgggccc	cac	gcgcgt	ctcag	ggagcg	ctct	ccgact	ccgc	acgggg	actc	gccaga	aaagg					2911
atcgtg	ac	gcatta	aatga	atcagg	gggat	aacgc	caggaa	agaac	atgtg	agcaaa	aggc					2971
cagcaaa	agg	ccagg	gaaccg	taaaa	aaggcc	gcgtt	gtctg	cg	tttttcca	tagg	ctccgc					3031
ccccctg	acg	agcat	cacaa	aaatc	gacgc	tcaag	tcaga	ggtgg	cgaaa	cccga	cagga					3091
ctataa	agat	accagg	cggt	tcccc	ctgga	agctccc	tcg	tgcgt	ctcc	tgttcc	gacc					3151
ctgcog	ctra	ccg	gatac	ct	gtccgc	cttt	ctccc	ttcgg	gaagc	gtggc	gcttt	ctcat				3211
agctc	acgct	gtagg	tatct	cagtt	cggtg	taggt	cgttc	gctcc	aagct	gggct	gtgtg					3271
cacga	acccc	ccgtt	cagcc	cgacc	gctgc	gc	ttatccg	gtaac	tatcg	tctt	gagtcc					3331
aacc	cggtaa	gacac	gactt	atcg	ccactg	gcag	cagcca	ctg	gtaac	ag	gattag	caga				3391
gcgag	gtatg	taggc	gggtgc	tacag	agttc	ttga	agtgg	ggc	ctaacta	cgg	ctac	act				3451
agaag	gacag	tattt	ggtat	ctgcg	ctctg	ctga	agccag	ttac	cttcgg	aaaa	agag	t				3511
ggtag	ctctt	gatcc	ggcaa	aca	aaccacc	gctg	gtagcg	gtg	gtttttt	tgtt	tgaag					3571
cagcag	atta	cgcg	cagaaa	aaa	aggatct	caaga	agatc	cttt	gatctt	ttct	acggg					3631
tctgac	gctc	agt	ggaacga	aaact	cacgt	taagg	gattt	tgg	catgag	attat	caaaa					3691
aggat	cttca	cctag	atcct	tttaa	aattaa	aat	gaag	tt	aaatca	at	ctaa	agtata				3751
tatgag	taaa	ctt	ggtctga	cag	ttaccaa	tgct	taata	ca	gtgagg	cacc	tatct	cagcg				3811
atctgt	ctat	ttc	gttcac	c	atagttg	cc	tgact	ccccg	tcgtg	tagat	aact	acgata				3871
cgggag	gggct	tacc	atctg	g	cccag	tgct	gcaat	gatac	cgcg	agaccc	acgct	caccg				3931
gctcc	agatt	tat	cagcaat	aaacc	agcca	gcc	ggaagg	g								

tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc gggtcccaac gatcaaggcg agttacatga 4171
 tcccccatgt tgtgcaaaaa agcgggttagc tcttcgggtc ctccgatcgt tgtcagaagt 4231
 aagttggccg cagtgttata actcatgggt atggcagcac tgcataattc tcttactgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgcctgc ggcgaccgag ttgtctctgc ccggcgctca caccgggataa taccgcgcca 4411
 catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca 4471
 aggatcttac cgtgtttgag atccagttcg atgtaaccca ctctgtcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct gggtgagcaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cctttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
 tagaaaaata aacaaaagag tttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771
 ctgcttaatt tgatgcctgg cagtttatgg cgggcgctct gcccgccacc ctccgggccc 4831
 ttgcttcgca acgttcaaat ccgctcccgg cggatttgct ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
 atgcctggca gttccctact ctcgcatggg gagacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgccaggca 5071
 aattcigtgt tatcagaccg cttctgcgtt ctgatttaac ctgtatcagg ctgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctagc ggccgata 5169

<210> 27

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3102

<400> 27

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110

20220220 10:22:00

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460

10073377-000000

```
<210> 28
<211> 5169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHL3103
```

<222> (191) .. (2461)

cccaaaaaaaaa aaaaaaaaaa aagagtccag agtggcccccg ccgctccgcg ccggggggggg 60

acaaagtgtc gcccggagta ctggtcgacc tccgaagtig ggggggagcg aaagcaaggca 180

aaccatttga atg gat gtc aat ccg act tta ctg ttc ttg aaa gtt cct 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gcg caa aat gca ata agt act acg ttc cct tac act gga gat cct cca 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

tac agc cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg .
30 35 40 45

aca cac caa tat tcg gaa aag ggg aaa tgg aca aca aac act gag act 373
Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa cca agt gga tat gca caa aca gac tgc gtc ctg gaa gca atg gct 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

ttc ctt gaa gaa tcc cat cca gga atc ttt gaa aac tcg tgt ctt gag 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu
95 100 105

acg atg gaa gtt gtt caa caa aca aga gtg gac aaa ctg acc caa ggc 565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
110 115 120 125

cgt cag act tat gat tgg act ttg aat aga aac cag cct gct gca act 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
130 135 140

gca tta gca aac act ata gag gtc ttt aga tcg aat ggt cta aca gct 661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
145 150 155

aat gaa tca ggg agg ctc ata gat ttc ctc aag gat gtg atg gaa tca 709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
160 165 170

atg gat aag gag gaa atg gag ata aca aca cat ttc caa cga aag aga 757
Met Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
175 180 185

aga gta aga gac aac atg acc aag aaa atg gtc aca caa aga aca ata 805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
190 195 200 205

ggg aag aaa aag cag aga ctt aac aaa agg agc tac cta ata agg gct 853
Gly Lys Lys Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
210 215 220

cta aca ttg aac aca atg acg aaa gat gca gaa aga ggt aaa ctg aag 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

aga aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr
 290 295 300

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtc ttg agc atc gcg ccg ata atg ttt tgc aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg
 350 355 360 365

aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met
 465 470 475

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

agc Ser	ttt Phe 495	ttc Phe	tat Tyr	cgt Arg	tat Tyr	ggg Gly 500	ttt Phe	gtt Val	gcc Ala	aat Asn 505	ttc Phe	agc Ser	atg Met	gag Glu	ctt Leu	1717
ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggt Gly 540	cca Pro	1813
gca Ala	acc Thr	gct Ala	caa Gln 545	atg Met	gcc Ala	ctt Leu	cag Gln	ctg Leu 550	ttc Phe	atc Ile	aaa Lys	gat Asp	tac Tyr 555	agg Arg	tac Tyr	1861
acg Thr	tac Tyr	cgg Arg 560	tgc Cys	cat His	aga Arg	ggg Gly	gac Asp 565	aca Thr	caa Gln	ata Ile	caa Gln	acc Thr 570	cga Arg	aga Arg	tca Ser	1909
ttt Phe 575	gaa Glu	ata Ile	aag Lys	aaa Lys	ctg Leu	tgg Trp 580	gag Glu	caa Gln	acc Thr	cat His 585	tcc Ser 585	aaa Lys	gct Ala	gga Gly	ctg Leu	1957
ctg Leu 590	gtc Val	tcc Ser	gac Asp	gga Gly	ggc Gly 595	cca Pro	aat Asn	tta Leu	tac Tyr 600	aac Asn	att Ile	aga Arg	aat Asn	ctc Leu	cac His 605	2005
att Ile	cct Pro	gaa Glu	gtc Val	tgc Cys 610	ttg Leu	aaa Lys	tgg Trp	gaa Glu	tta Leu 615	atg Met	gat Asp	gag Glu	gat Asp	tac Tyr 620	cag Gln	2053
ggg Gly	cgt Arg	tta Leu	tgc Cys 625	aac Asn	cca Pro	ctg Leu	aac Asn	cca Pro 630	ttt Phe	gtc Val	aac Asn	cat His	aaa Lys 635	gac Asp	att Ile	2101
gaa Glu	tca Ser 640	gtg Val	aac Asn	aat Asn	gca Ala	gtg Val	ata Ile 645	atg Met	cca Pro	gca Ala	cat His 650	ggt Gly 650	cca Pro	gcc Ala	aaa Lys	2149
aac Asn	atg Met 655	gag Glu	tat Tyr	gat Asp	gct Ala	gtt Val 660	gca Ala	aca Thr	aca Thr	cac His	tcc Ser 665	tgg Trp	atc Ile	ccc Pro	aaa Lys	2197
aga Arg 670	aat Asn	cga Arg	tcc Ser	atc Ile	ttg Leu 675	aat Asn	aca Thr	agc Ser	caa Gln	aga Arg 680	gga Gly	ata Ile	ctt Leu	gaa Glu	gat Asp 685	2245
gaa Glu	caa Gln	atg Met	tac Tyr 690	caa Gln	aag Lys	tgc Cys	tgc Cys	aac Asn 695	tta Leu 695	ttt Phe	gaa Glu	aaa Lys	ttc Phe 700	ttc Phe 700	ccc Pro	2293
agc Ser	agt Ser	tca Ser	tac Tyr 705	aga Arg	aga Arg	cca Pro	gtc Val	ggg Gly 710	ata Ile	tcc Ser	agt Ser	atg Met	gtg Val 715	gag Glu	gct Ala	2341
atg Met	gtt Val	tcc Ser 720	aga Arg	gcc Ala	cga Arg	att Ile	gat Asp 725	gca Ala	cga Arg	att Ile	gat Asp 730	ttc Phe 730	gaa Glu	tct Ser	gga Gly	2389
agg Arg	ata Ile 735	aag Lys	aaa Lys	gag Glu	gag Glu	ttc Phe 740	act Thr	gag Glu	atc Ile	atg Met	aag Lys 745	atc Ile	tgt Cys	tcc Ser	acc Thr	2437

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

atgccttgtt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611
 cacggacacc tgtccccaaa aacgccacca tcgcagccac acacggagcg ccgggggccc 2671
 tctggtcaac ccaggacac acgcgggagc agcgccgggc cggggacgcc ctcccggccg 2731
 cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggccccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggcccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa ccgcacagga 3091
 ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttccgacc 3151
 ctgcgcctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcgggt taggtcggtc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331
 aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcggtgc tacagagttc ttgaagtggg ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtgggttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacggg 3631
 tctgacgctc agtggaacga aaactcacgt taagggattt tggatcatgag attatcaaaa 3691
 aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataaat ctaaagtata 3751
 tatgagtaaa cttggtctga cagttaccaa tgcttaatca gtgaggcacc tatctcagcg 3811
 atctgtctat ttcgttcac ctagttgcc tgactccccg tcgtgtagat aactacgata 3871
 cgggagggct taccatctgg cccagtggt gcaatgatac cgcgagacc acgctcaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgag aagtggctct 3991
 gcaactttat ccgcctccat ccagttctatt aattgttgcc gggaagctag agtaagtagt 4051
 tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc gggtcccaac gatcaaggcg agttacatga 4171
 tccccatgt tgtgcaaaaa agcgggttagc tccttcggtc ctccgatcgt tgtcagaagt 4231
 aagttggccg cagtgttatc actcatggtt atggcagcac tgcataattc tcttactgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgtatgc ggccagccag ttgctcttgc ccggcgtaaa cacgggataa taccgcgcca 4411

200207252007

catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca 4471
 aggatcttac cgctgttgag atccagttcg atgtaaccca ctctgtgcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct ggggtgagcaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cctttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
 tagaaaaata aacaaaagag tttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771
 ctgtttaatt tgatgectgg cagtttatgg cgggcgtcct gcccgccacc ctccggggcg 4831
 ttgcttcgca acgttcaaat ccgctcccgg cggatttgct ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
 atgectggca gttccctact ctgcgatggg gagacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgccaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctagc ggccgatac 5169

<210> 29
 <211> 757
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: pHL3103

<400> 29
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
 1 5 10 15
 Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
 20 25 30
 Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45
 Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asp Lys
 165 170 175

1007337.020302

Glu 180	Glu 181	Met 182	Ile 183	Thr 184	Thr 185	His 186	Phe 187	Gln 188	Arg 189	Lys 190	Arg 191	Val 192	Arg 193	Val 194	Arg 195
Asp 196	Asn 197	Met 198	Thr 199	Lys 200	Lys 201	Met 202	Val 203	Thr 204	Gln 205	Arg 206	Thr 207	Ile 208	Gly 209	Lys 210	Lys 211
Lys 212	Gln 213	Arg 214	Leu 215	Asn 216	Lys 217	Arg 218	Ser 219	Tyr 220	Leu 221	Ile 222	Arg 223	Ala 224	Leu 225	Thr 226	Leu 227
Asn 228	Thr 229	Met 230	Thr 231	Lys 232	Asp 233	Ala 234	Glu 235	Arg 236	Gly 237	Lys 238	Leu 239	Lys 240	Arg 241	Arg 242	Ala 243
Ile 244	Ala 245	Thr 246	Pro 247	Gly 248	Met 249	Gln 250	Ile 251	Arg 252	Gly 253	Phe 254	Val 255	Tyr 256	Phe 257	Val 258	Glu 259
Thr 260	Leu 261	Ala 262	Arg 263	Ser 264	Ile 265	Cys 266	Glu 267	Lys 268	Leu 269	Glu 270	Gln 271	Ser 272	Gly 273	Leu 274	Pro 275
Val 276	Gly 277	Gly 278	Asn 279	Glu 280	Lys 281	Lys 282	Ala 283	Lys 284	Leu 285	Ala 286	Asn 287	Val 288	Val 289	Arg 290	Lys 291
Met 292	Met 293	Thr 294	Asn 295	Ser 296	Gln 297	Asp 298	Thr 299	Glu 300	Leu 301	Ser 302	Phe 303	Thr 304	Ile 305	Thr 306	Gly 307
Asp 308	Asn 309	Thr 310	Lys 311	Trp 312	Asn 313	Glu 314	Asn 315	Gln 316	Asn 317	Pro 318	Arg 319	Met 320	Phe 321	Leu 322	Ala 323
Met 324	Ile 325	Thr 326	Tyr 327	Ile 328	Thr 329	Arg 330	Asn 331	Gln 332	Pro 333	Glu 334	Trp 335	Phe 336	Arg 337	Asn 338	Val 339
Leu 340	Ser 341	Ile 342	Ala 343	Pro 344	Ile 345	Met 346	Phe 347	Ser 348	Asn 349	Lys 350	Met 351	Ala 352	Arg 353	Leu 354	Gly 355
Lys 356	Gly 357	Tyr 358	Met 359	Phe 360	Glu 361	Ser 362	Lys 363	Ser 364	Met 365	Lys 366	Leu 367	Arg 368	Thr 369	Gln 370	Ile 371
Pro 372	Ala 373	Glu 374	Met 375	Leu 376	Ala 377	Ser 378	Ile 379	Asp 380	Leu 381	Lys 382	Tyr 383	Phe 384	Asn 385	Glu 386	Pro 387
Thr 388	Arg 389	Lys 390	Lys 391	Ile 392	Glu 393	Lys 394	Ile 395	Arg 396	Pro 397	Leu 398	Ile 399	Ile 400	Asp 401	Gly 402	Thr 403
Ala 404	Ser 405	Leu 406	Ser 407	Pro 408	Gly 409	Met 410	Met 411	Met 412	Gly 413	Met 414	Phe 415	Asn 416	Met 417	Leu 418	Ser 419
Thr 420	Val 421	Leu 422	Gly 423	Val 424	Ser 425	Ile 426	Leu 427	Asn 428	Leu 429	Gly 430	Gln 431	Lys 432	Arg 433	Tyr 434	Thr 435
Lys 436	Thr 437	Thr 438	Tyr 439	Trp 440	Trp 441	Asp 442	Gly 443	Leu 444	Gln 445	Ser 446	Ser 447	Asp 448	Asp 449	Phe 450	Ala 451
Leu 452	Ile 453	Val 454	Asn 455	Ala 456	Pro 457	Asn 458	His 459	Glu 460	Gly 461	Ile 462	Gln 463	Ala 464	Gly 465	Val 466	Asp 467
Arg 468	Phe 469	Tyr 470	Arg 471	Thr 472	Cys 473	Lys 474	Leu 475	Val 476	Gly 477	Ile 478	Asn 479	Met 480	Ser 481	Lys 482	Lys 483
Lys 484	Ser 485	Tyr 486	Ile 487	Asn 488	Arg 489	Thr 490	Gly 491	Thr 492	Phe 493	Glu 494	Phe 495	Thr 496	Ser 497	Phe 498	Phe 499
Tyr 500	Arg 501	Tyr 502	Gly 503	Phe 504	Val 505	Ala 506	Asn 507	Phe 508	Ser 509	Met 510	Glu 511	Leu 512	Pro 513	Ser 514	Phe 515
Gly 516	Val 517	Ser 518	Gly 519	Ile 520	Asn 521	Glu 522	Ser 523	Ala 524	Asp 525	Met 526	Ser 527	Ile 528	Gly 529	Val 530	Tnr 531

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
565 570 575

Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

<210> 3C
<211> 5169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHL3130

<220>
<221> CDS
<222> (191)..(2461)

<400> 30
cccaaaaaaa aaaaaaaaaa aagagtccag agtggccccc cgcctccgcg ccgggggggg 60
gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
Thr Met Glu Val Val Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
225 230 235

cgg aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac 949
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
240 245 250

ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct 997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
255 260 265

100737-020000

ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val 285
 270 275 280

gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr 300
 290 295

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 315
 305 310

ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe 330
 320 325

aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala 345
 335 340

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg 365
 350 355 360

aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 380
 370 375

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile 395
 385 390

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 410
 400 405

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 425
 415 420

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 445
 430 435 440

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 460
 450 455

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met 475
 465 470

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr 490
 480 485

agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu 505
 495 500

ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 525
 510 515 520

20220420 16:20:00

gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu
 575 580 585

ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac 2003
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att 2101
 Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile
 625 630 635

gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys
 640 645 650

agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag 2197
 Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat 2243
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

agc agc tca tac aga aga cca gtt gga att tcc agt atg gtg gag gcc 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715

atg gtg tct agg gcc cgg att gat gca cga att gac ttc gag tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgctct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

atgccttggt tctactaata acccggcggc ccaaatgcc gactcggagc gaaagatata 2551

cctcccccg ggccgggagg tcgcgtcacc gaccacgcc cgggcccagg cgacgcgcga 2611

cacggacacc tgtccccaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671

tctggtcaac ccaggacac acgcgggagc agcgcggggc cggggacgcc ctcccggccg 2731

1007337 020000

ccggtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggcccgar gcgcgctrag ggagcgcctc ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacaatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091
 ctataaagat accaggcgtt tccccctgga agctccctcg tgcgctctcc tgttccgacc 3151
 ctgccgttta ccgataacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcgggtg taggtcgttc gctccaagct gggctgtgtg 3271
 caccgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331
 aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcggtgc tacagagttc ttgaagtggc ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaacacc cctggtagcg gtggtttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
 tctgacgctc agtggaaacga aaactcacgt taagggattt tggcatgag attatcaaaa 3691
 aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataaat ctaaagtata 3751
 tatgagtaaa cttggtctga cagttaccaa tgcttaatca gtgaggcacc tatctcagcg 3811
 atctgtctat ttctgtctac catagttgcc tgactccccg tcgtgtagat aactacgata 3871
 cgggaggggt taccatctgg cccagtgct gcaatgatac cgcgagaccc acgctcaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgcag aagtggctct 3991
 gcaactttat ccgcctccat ccagtctatt aattgttgcc ggaagctag agtaagtagt 4051
 tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc ggttcccaac gatcaaggcg agttacatga 4171
 tccccatgt tgtgcaaaaa agcggtttagc tccttcggtc ctccgatcgt tgtcagaagt 4231
 aagttggccg cagtgttatc actcatggtt atggcagcac tgcataattc tcttactgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgatgc ggcgaccgag ttgctcttgc ccggcgtcaa cacgggataa taccgcgcca 4411
 catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca 4471
 aggatcttac cgctgttgag atccagttcg atgtaacca ctctgcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct gggtagacaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaaatac tcataactctt cctttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711

100337.00800


```
<210> 31
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3130

<400> 31
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
  1                               5                      10          15
Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
                20                        25              30
Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
      35                                40                  45
Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
    50                             55              60
Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
  65                          70                   75           80
Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
                    85                            90          95
Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
        100                       105             110
Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
   115                         120                 125
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
   130                     135               140
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
  145                 150                   155           160
Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
            165                         170              175
Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
       180                           185               190
Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
   195                     200              205
Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
   210                 215                   220
```

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575

100337-02000

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 32
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3131

<220>
 <221> CDS
 <222> (191)..(2461)

<400> 32
 cccaaaaaaa aaaaaaaaaa aagagtccag agtggccccc ccgctccgcg ccgggggggg 60
 gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
 acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10
 gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25
 tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

1007337.000000

aca	cat	cag	tac	tca	gaa	agg	gga	aga	tgg	aca	aca	aac	acc	gaa	act	373
Thr	His	Gln	Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	
				50					55					60		
gga	gca	ccg	caa	ctc	aac	ccg	att	gat	ggg	cca	ctg	cca	gaa	gac	aat	421
Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	
			65					70					75			
gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	
		80					85					90				
ttc	ctt	gag	gaa	tcc	cat	cct	ggt	atc	ttt	gag	acc	tcg	tgt	ctt	gaa	517
Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	
	95					100					105					
acg	atg	gag	gtt	gtt	cag	caa	aca	cga	gtg	gac	aag	ctg	aca	caa	ggc	565
Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	
110					115				120						125	
cga	cag	acc	tat	gac	tgg	act	cta	aat	agg	aac	cag	cct	gct	gca	aca	613
Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	
				130					135					140		
gca	ttg	gcc	aac	aca	ata	gaa	gtg	ttc	aga	tca	aat	ggc	ctc	acg	gcc	661
Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	
			145					150					155			
aat	gaa	tct	gga	agg	ctc	ata	gac	ttc	ctt	aag	gat	gta	atg	gag	tca	709
Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
		160					165					170				
atg	aac	aaa	gaa	gaa	atg	gag	atc	aca	act	cat	ttt	cag	aga	aag	aga	757
Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
	175					180					185					
cga	gtg	aga	gac	aat	atg	act	aag	aaa	atg	gtg	aca	cag	aga	aca	ata	805
Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
190					195					200					205	
ggt	aaa	agg	aag	cag	aga	ttg	aac	aaa	agg	agt	tat	cta	att	agg	gca	853
Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
				210					215					220		
tta	acc	ctg	aac	aca	atg	acc	aaa	gat	gct	gag	aga	ggg	aag	cta	aaa	901
Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
			225					230					235			
cgg	aga	gca	att	gca	aca	cca	ggg	atg	cag	atc	aga	ggg	ttt	gtg	tac	949
Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	
		240					245					250				
ttt	gtt	gag	aca	ctg	gcg	aga	agc	att	tgc	gag	aag	ctt	gaa	cag	tct	997
Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
	255					260					265					
ggg	cta	cca	gtt	gga	ggg	aat	gag	aag	aaa	gct	aaa	ttg	gca	aat	gtc	1045
Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	
270					275					280					285	
gtg	agg	aag	atg	atg	acg	aac	tca	caa	gac	act	gag	ctc	tct	ttc	aca	1093
Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	Ser	Phe	Thr	
					290				295					300		

10073377-00000000

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg	1141
Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met	
305 310 315	
ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt	1189
Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe	
320 325 330	
aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg	1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala	
335 340 345	
agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga	1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg	
350 355 360 365	
aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc	1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe	
370 375 380	
aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata	1381
Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile	
385 390 395	
gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac	1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn	
400 405 410	
atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag	1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat	1525
Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp	
430 435 440 445	
gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg	1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg	1621
Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca	1669
Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac	1861
Ala Thr Ala Gln Met Ala Leu Gln Phe Ile Lys Asp Tyr Arg Tyr	
545 550 555	
acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	

10073377-020003

ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
 Gly Arg Ile Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
 625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
 640 645 650

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2197
 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715

atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551

cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611

cacggacacc tgtccccaaa aacgccacca tcgcagccac acacggagcg ccggggggccc 2671

tctggtcaac ccaggacac acgcgggagc agcgcggggc cggggacgcc ctccgggccg 2731

cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791

gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851

cgggcccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911

atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971

cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031

cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091

10073377-0208002
 20080207-0208002

ctataaagat	accaggcggtt	tccccctgga	agctccctcg	tgcgctctcc	tggtccgacc	3151
ctgccgctta	coggatacct	gtccgccttt	ctcccttcgg	gaagcgtggc	gctttctcat	3211
agctcacgt	gtaggatat	cagttcgggtg	taggtcggtt	gctccaagct	gggctgtgtg	3271
cacgaacccc	cgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tcttgagtc	3331
aacccggtaa	gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gattagcaga	3391
gcgaggcatg	taggcgggtgc	tacagagttc	ttgaagtgg	ggcctaacta	cggctacact	3451
agaaggacag	tatttggtat	ctgcgctctg	ctgaagccag	ttaccttcgg	aaaaagagtt	3511
ggtagctctt	gatccggcaa	acaaaccacc	gctggtagcg	gtggtttttt	tgtttgcaag	3571
cagcagatta	cgcgcagaaa	aaaaggatct	caagaagatc	ctttgatctt	ttctacgggg	3631
tctgacgctc	agtggaacga	aaactcacgt	taagggattt	tggtcatgag	attatcaaaa	3691
aggatcttca	cctagatcct	tttaaattaa	aatgaagtt	ttaaatcaat	ctaaagtata	3751
tatgagtaaa	cttgggtctga	cagttaccaa	tgcttaatca	gtgaggcacc	tatctcagcg	3811
atctgtctat	ttcgttcatc	catagttgcc	tgactccccg	tcgtgtagat	aactacgata	3871
cgggagggct	taccatctgg	ccccagtgt	gcaatgatac	cgcgagaccc	acgtccaccg	3931
gctccagatt	tatcagcaat	aaaccagcca	gccggaagg	ccgagcgcag	aagtggctct	3991
gcaactttat	ccgcctccat	ccagtctatt	aattgttgcc	gggaagctag	agtaagtagt	4051
tcgccagtta	atagtttgcg	caacgttggt	gccattgcta	caggcatcgt	ggtgtcacgc	4111
tcgtcgtttg	gtatggcttc	attcagctcc	ggttcccaac	gatcaaggcg	agttacatga	4171
tcccccatgt	tgtgcaaaaa	agcgggttagc	tccttcggtc	ctccgatcgt	tgtcagaagt	4231
aagttggccg	cagtgttata	actcatgggt	atggcagcac	tgcataattc	tcttactgtc	4291
atgccatccg	taagatgctt	ttctgtgact	ggtgagtact	caaccaagtc	attctgagaa	4351
tagtgtatgc	ggcgaccgag	ttgtctttgc	ccggcgtaaa	cacgggataa	taccgcgcc	4411
catagcagaa	ctttaaaagt	gctcatcatt	ggaaaacgtt	cttcggggcg	aaaactctca	4471
aggatcttac	cgtgttgag	atccagttcg	atgtaacca	ctcgtgcacc	caactgatct	4531
tcagcatctt	ttactttcac	cagcgtttct	gggtgagcaa	aaacaggaag	gcaaaatgcc	4591
gcaaaaaagg	gaataagggc	gacacggaaa	tggtgaatac	tcatactctt	cctttttcaa	4651
tattatigaa	gcatttatca	gggttattgt	ctcatgagcg	gatacatatt	tgaatgtatt	4711
tagaaaaata	aacaaaagag	tttgtagaaa	cgcaaaaagg	ccatccgtca	ggatggcctt	4771
ctgcttaatt	tgatgcctgg	cagtttatgg	cgggcgtcct	gcccgccacc	ctccggggcg	4831
ttgcttcgca	acgttcaaat	ccgtccccgg	cggatttgtc	ctactcagga	gagcgttcac	4891
cgacaaacaa	cagataaaac	gaaaggccca	gtctttcgac	tgagcctttc	gttttatttg	4951
atgcctggca	gttccttact	ctcgcattgg	gagacccac	actaccatcg	gcgctacggc	5011
gtttcacttc	tgagttcggc	atggggtcag	gtgggaccac	cgcgctactg	ccgccaggca	5071

```
<210> 33
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3131
```

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
340 345 350

Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
355 360 365

Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
370 375 380

Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
385 390 395 400

Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
405 410 415

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
420 425 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
435 440 445

Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
565 570 575

Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
625 630 635 640

10073377-00000000

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

<210> 34
<211> 5169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHL3203

<220>
<221> CDS
<222> (191)..(2461)

<400> 34
cccaaaaaaaaa aaaaaaaaaa aagagtccag agtggcccccg ccgctccgcg ccggggggggg 60
ggggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

20220722 16:00

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca tgg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

20250207 14:22:00

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg 365
 350 355 360 365

 act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 380
 370 375

 aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
 Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile 395
 385 390 395

 gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 410
 400 405 410

 atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 425
 415 420 425

 aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat 1525
 Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 445
 430 435 440 445

 gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 460
 450 455 460

 gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg 1621
 Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met 475
 465 470 475

 agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr 490
 480 485 490

 agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu 505
 495 500 505

 ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 525
 510 515 520 525

 gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro 540
 530 535 540

 gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr 555
 545 550 555

 acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser 570
 560 565 570

 ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu 585
 575 580 585

 ctg gtc tcc gac gga ggc cca aat ttg tac aac att cgg aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 605
 590 595 600 605

 atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 620
 610 615 620

20250420 15:00:00

gga Gly	aga Arg	ctt Leu	tgt Cys 625	aat Asn	ccc Pro	atg Met	aac Asn	ccg Pro 630	ttt Phe	gtc Val	agt Ser	cat His	aag Lys 635	gaa Glu	att Ile	2101					
gaa Glu	tct Ser	gta Val 640	aac Asn	aat Asn	gct Ala	gcg Ala 645	gta Val	atg Met	cca Pro	gcc Ala	cat His	ggt Gly 650	cca Pro	gcc Ala	aaa Lys	2149					
agc Ser	atg Met 655	gaa Glu	tat Tyr	gat Asp	gct Ala 660	gtg Val 660	gca Ala	act Thr	aca Thr	cac His	tct Ser 665	tgg Trp	atc Ile	cct Pro	aag Lys	2197					
aga Arg 670	aac Asn	cgt Arg	tcc Ser	att Ile	ctc Leu 675	aat Asn	acg Thr	agt Ser	caa Gln	agg Arg 680	gga Gly	atc Ile	ctt Leu	gag Glu	gat Asp 685	2245					
gaa Glu	caa Gln	atg Met	tac Tyr 690	cag Gln	aag Lys	tgt Cys	tgc Cys	aac Asn 695	cta Leu	ttc Phe	gag Glu	aaa Lys	ttc Phe 700	ttc Phe	cct Pro	2293					
agc Ser	agc Ser	tca Ser 705	tac Tyr	aga Arg	aga Arg	cca Pro	gtt Val	gga Gly 710	att Ile	tcc Ser	agt Ser	atg Met	gtg Val 715	gag Glu	gcc Ala	2341					
atg Met	gtg Val	tct Ser 720	agg Arg	gcc Ala	cgg Arg	att Ile	gat Asp 725	gca Ala	cga Arg	att Ile	gac Asp	ttc Phe 730	gag Glu	tct Ser	gga Gly	2389					
agg Arg 735	att Ile	aag Lys	aag Lys	gaa Glu	gag Glu	ttt Phe 740	gct Ala	gag Glu	atc Ile	atg Met	aag Lys 745	atc Ile	tgt Cys	tcc Ser	acc Thr	2437					
att Ile 750	gaa Glu	gag Glu	ctc Leu	aga Arg	cgg Arg 755	caa Gln	aaa Lys	tagtgaattt	agcttgtcct	tcatgaaaaa	2491										
atgccttggtt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551																					
cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611																					
cacggacacc tgtcccaaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671																					
tctggtcaac ccaggacac acgcgggagc agcgccgggc cggggacgcc ctcccggccg 2731																					
cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791																					
gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851																					
cgggccgcac gcgcgctcag ggagcgctct ccgactccgc acgggggactc gccagaaagg 2911																					
atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971																					
cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031																					
ccccctgacg agcatcacaa aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091																					
ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttcgacc 3151																					
ctgccgctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211																					
agctcacgct gtaggtatct cagttcggtg taggtcgttc gctccaagct gggctgtgtg 3271																					
cacgaac																					

gcgaggtatg taggcggtgc tacagagttc ttgaagtggg ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
 tctgagctc agtggaacga aaactcacgt taagggattt tggcatgag attatcaaaa 3691
 aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataaat ctaaagtata 3751
 tatgagtaaa cttggtctga cagttaccaa tgcttaataca gtgaggcacc tatctcagcg 3811
 atctgtctat ttggttcac catagttgcc tgactccccg tcgtgtagat aactacgata 3871
 cgggaggggt taccatctgg cccagtggt gcaatgatac cgcgagaccc acgctcaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgcag aagtggctct 3991
 gcaactttat ccgcctccat ccagttctatt aattgttgcc ggaagctag agtaagtagt 4051
 tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc gggtcccaac gatcaaggcg agttacatga 4171
 tccccatgt tgtgcaaaaa agcgggttagc tccttcggtc ctccgatcgt tgtcagaagt 4231
 aagttggccg cagtgttacc actcatggtt atggcagcac tgcataattc tcttactgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgtatgc ggcgaccgag ttgctcttgc ccggcgtaaa cacgggataa taccgcgcca 4411
 catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca 4471
 aggatcttac cgctgttgag atccagttcg atgtaacca ctcgtgcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct gggtgagcaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cctttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
 tagaaaaata aacaaaagag tttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771
 ctgcttaatt tgatgcctgg cagtttatgg cgggcgtcct gcccgccacc ctccggggcg 4831
 ttgcttcgca acgttcaaat ccgctcccg cggatttgtc ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
 atgcctggca gttccctact ctgcgatggg gagacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgtactg ccgccaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctagc ggccgatc 5169

<210> 35

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3203

20250720 16:20:00

Met 1	Asp	Val	Asn	Pro 5	Thr	Leu	Leu	Phe	Leu 10	Lys	Val	Pro	Ala	Gln 15	Asn
Ala	Ile	Ser	Thr 20	Thr	Phe	Pro	Tyr	Thr 25	Gly	Asp	Pro	Pro	Tyr 30	Ser	His
Gly	Thr	Gly 35	Thr	Gly	Tyr	Thr	Met 40	Asp	Thr	Val	Asn 45	Arg	Thr	His	Gln
Tyr	Ser 50	Glu	Arg	Gly	Arg	Trp 55	Thr	Thr	Asn	Thr	Glu 60	Thr	Gly	Ala	Pro
Gln 65	Leu	Asn	Pro	Ile	Asp 70	Gly	Pro	Leu	Pro	Glu 75	Asp	Asn	Glu	Pro	Ser 80
Gly	Tyr	Ala	Gln	Thr 85	Asp	Cys	Val	Leu	Glu 90	Ala	Met	Ala	Phe	Leu 95	Glu
Glu	Ser	His	Pro 100	Gly	Ile	Phe	Glu	Thr 105	Ser	Cys	Leu	Glu	Thr 110	Met	Glu
Val	Val	Gln 115	Gln	Thr	Arg	Val	Asp 120	Lys	Leu	Thr	Gln	Gly 125	Arg	Gln	Thr
Tyr	Asp 130	Trp	Thr	Leu	Asn 135	Arg	Asn	Gln	Pro	Ala	Ala 140	Thr	Ala	Leu	Ala
Asn 145	Thr	Ile	Glu	Val	Phe 150	Arg	Ser	Asn	Gly	Leu 155	Thr	Ala	Asn	Glu	Ser 160
Gly	Arg	Leu	Ile	Asp 165	Phe	Leu	Lys	Asp	Val 170	Met	Glu	Ser	Met	Asn 175	Lys
Glu	Glu	Met	Glu 180	Ile	Thr	Thr	His	Phe 185	Gln	Arg	Lys	Arg	Arg 190	Val	Arg
Asp	Asn	Met 195	Thr	Lys	Lys	Met	Val 200	Thr	Gln	Arg	Thr	Ile 205	Gly	Lys	Arg
Lys	Gln 210	Arg	Leu	Asn	Lys	Arg 215	Ser	Tyr	Leu	Ile	Arg 220	Ala	Leu	Thr	Leu
Asn 225	Thr	Met	Thr	Lys	Asp 230	Ala	Glu	Arg	Gly	Lys 235	Leu	Lys	Arg	Arg	Ala 240
Ile	Ala	Thr	Pro	Gly 245	Met	Gln	Ile	Arg	Gly 250	Phe	Val	Tyr	Phe	Val 255	Glu
Thr	Leu	Ala	Arg 260	Ser	Ile	Cys	Glu	Lys 265	Leu	Glu	Gln	Ser	Gly 270	Leu	Pro
Val	Gly	Gly 275	Asn	Glu	Lys	Lys	Ala 280	Lys	Leu	Ala	Asn	Val 285	Val	Arg	Lys
Met	Met 290	Thr	Asn	Ser	Gln	Asp 295	Thr	Glu	Ile	Ser	Phe 300	Thr	Ile	Thr	Gly
Asp 305	Asn	Thr	Lys	Trp	Asn 310	Glu	Asn	Gln	Asn	Pro 315	Arg	Met	Phe	Leu	Ala 320
Met	Ile	Thr	Tyr	Ile 325	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335	Val
Leu	Ser	Ile	Ala 340	Pro	Ile	Met	Phe	Ser 345	Asn	Lys	Met	Ala	Arg 350	Leu	Gly

Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

1007337-622200
 200809-222000

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

<210> 36

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3204

<220>

<221> CDS

<222> (191)..(2461)

<400> 36

```

ccccaaaaaaaa aagagtcacg agtggccccc cgcctccgcg ccggggggggg 60
ggggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
      Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
      1 5 10
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
      15 20 25
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
      30 35 40 45
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
      50 55 60
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
      65 70 75
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
      80 85 90
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
      95 100 105
acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
      110 115 120 125
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
      130 135 140

```

1007337-22000

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
 350 355 360 365

act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
 Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile
 385 390 395

100337.000000

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat	1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn	
400 405 410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag	1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat	1525
Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp	
430 435 440 445	
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc	1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg	1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca	1669
Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat	1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr	
545 550 555	
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	
ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg	1957
Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu	
575 580 585	
ttg gtt tca gat ggc gga cca aac ctg tac aac att aga aat ctc cac	2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His	
590 595 600 605	
att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag	2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln	
610 615 620	
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att	2101
Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile	
625 630 635	
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa	2149
Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys	
640 645 650	
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa	2197
Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys	
655 660 665	

1007337-020802

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat	2245
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp	
670 675 680 685	
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc	2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro	
690 695 700	
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct	2341
Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala	
705 710 715	
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga	2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly	
720 725 730	
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc	2437
Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr	
735 740 745	
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgctcct tcatgaaaaa	2491
Ile Glu Glu Leu Arg Arg Gln Lys	
750 755	
atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata	2551
cctcccccg ggccgggagg tcgcgtcacc gaccacgcc cgggccagg cgacgcgcga	2611
cacggacacc tgtccccaaa aacgccacca tcgcagccac acacggagcg cccggggccc	2671
tctggtcaac ccaggacac acgcgggagc agcgcggggc cggggacgcc ctccgggccg	2731
cccggtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg	2791
gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct	2851
cggggccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg	2911
atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc	2971
cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc	3031
ccccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga	3091
ctataaagat accaggcggt tccccctgga agctccctcg tcgcgtctcc tgttccgacc	3151
ctgccgctta ccgatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat	3211
agctcacgct gtaggtatct cagttcgggt taggtcgttc gctccaagct gggctgtgtg	3271
cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtc	3331
aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga	3391
gcgaggtatg taggcgggtgc tacagagttc ttgaagtggg ggcctaacta cggctacact	3451
agaaggacag tatttggrat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt	3511
ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag	3571
cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg	3631
tctgacgctc agtggaacga aaactcacgt taagggattt tggtcatgag attatcaaaa	3691
aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaatcaat ctaaagtata	3751

```
<210> 37
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3204
```

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln 65	Leu	Asn	Pro	Ile	Asp 70	Gly	Pro	Leu	Pro	Glu 75	Asp	Asn	Glu	Pro	Ser 80
Gly	Tyr	Ala	Gln	Thr 85	Asp	Cys	Val	Leu	Glu 90	Ala	Met	Ala	Phe	Leu 95	Glu
Glu	Ser	His	Pro 100	Gly	Ile	Phe	Glu	Thr 105	Ser	Cys	Leu	Glu	Thr 110	Met	Glu
Val	Val	Gln 115	Gln	Thr	Arg	Val	Asp 120	Lys	Leu	Thr	Gln	Gly 125	Arg	Gln	Thr
Tyr	Asp 130	Trp	Thr	Leu	Asn	Arg 135	Asn	Gln	Pro	Ala	Ala 140	Thr	Ala	Leu	Ala
Asn 145	Thr	Ile	Glu	Val	Phe 150	Arg	Ser	Asn	Gly	Leu 155	Thr	Ala	Asn	Glu	Ser 160
Gly	Arg	Leu	Ile	Asp 165	Phe	Leu	Lys	Asp	Val 170	Met	Glu	Ser	Met	Asn 175	Lys
Glu	Glu	Met	Glu 180	Ile	Thr	Thr	His	Phe 185	Gln	Arg	Lys	Arg	Arg 190	Val	Arg
Asp	Asn	Met 195	Thr	Lys	Lys	Met	Val 200	Thr	Gln	Arg	Thr	Ile 205	Gly	Lys	Arg
Lys	Gln 210	Arg	Leu	Asn	Lys	Arg 215	Ser	Tyr	Leu	Ile	Arg 220	Ala	Leu	Thr	Leu
Asn 225	Thr	Met	Thr	Lys	Asp 230	Ala	Glu	Arg	Gly	Lys 235	Leu	Lys	Arg	Arg	Ala 240
Ile	Ala	Thr	Pro	Gly 245	Met	Gln	Ile	Arg	Gly 250	Phe	Val	Tyr	Phe	Val 255	Glu
Thr	Leu	Ala	Arg 260	Ser	Ile	Cys	Glu	Lys 265	Leu	Glu	Gln	Ser	Gly 270	Leu	Pro
Val	Gly	Gly 275	Asn	Glu	Lys	Lys	Ala 280	Lys	Leu	Ala	Asn	Val 285	Val	Arg	Lys
Met	Met 290	Thr	Asn	Ser	Gln	Asp 295	Thr	Glu	Ile	Ser	Phe 300	Thr	Ile	Thr	Gly
Asp 305	Asn	Thr	Lys	Trp	Asn 310	Glu	Asn	Gln	Asn	Pro 315	Arg	Met	Phe	Leu	Ala 320
Met	Ile	Thr	Tyr 325	Ile	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335	Val
Leu	Ser	Ile	Ala 340	Pro	Ile	Met	Phe	Ser 345	Asn	Lys	Met	Ala	Arg 350	Leu	Gly
Lys	Gly	Tyr 355	Met	Phe	Glu	Ser	Lys 360	Ser	Met	Lys	Ile	Arg 365	Thr	Gln	Ile
Pro	Ala 370	Glu	Met	Leu	Ala	Ser 375	Ile	Asp	Leu	Lys	Tyr 380	Phe	Asn	Asp	Ser
Thr 385	Arg	Lys	Lys	Ile	Glu 390	Lys	Ile	Arg	Pro	Leu 395	Leu	Ile	Asp	Gly	Thr 400
Ala	Ser	Leu	Ser	Pro 405	Gly	Met	Met	Met	Gly 410	Met	Phe	Asn	Met	Leu 415	Ser

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

1007337-000000

[illegible]

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr
 290 295 300

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg
 350 355 360 365

aca caa ata cca gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
 Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile
 385 390 395

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat 1525
 Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

1007997
 2000000

gga Gly	gtc Val	aac Asn	agg Arg 465	ttt Phe	tat Tyr	cga Arg	acc Thr	tgt Cys 470	aag Lys	cta Leu	ctt Leu	gga Gly	att Ile 475	aat Asn	atg Met	1621
agc Ser	aag Lys	aaa Lys 480	aag Lys	tct Ser	tac Tyr	ata Ile	aac Asn 485	aga Arg	aca Thr	ggt Gly	aca Thr	ttt Phe 490	gaa Glu	ttc Phe	aca Thr	1669
agc Ser	ttt Phe 495	ttc Phe	tat Tyr	cgt Arg	tat Tyr	ggg Gly 500	ttt Phe	gtt Val	gcc Ala	aat Asn	ttc Phe 505	agc Ser	atg Met	gag Glu	ctt Leu	1717
ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggg Gly 540	cca Pro	1813
gca Ala	acc Thr	gct Ala	caa Gln 545	atg Met	gcc Ala	ctt Leu	cag Gln	ctg Leu 550	ttc Phe	atc Ile	aaa Lys	gat Asp 555	tac Tyr 555	agg Arg	tac Tyr	1861
acg Thr	tac Tyr	cgg Arg 560	tgc Cys	cat His	aga Arg	ggg Gly	gac Asp 565	aca Thr	caa Gln	ata Ile	caa Gln	acc Thr 570	cga Arg	aga Arg	tca Ser	1909
ttt Phe	gaa Glu 575	ata Ile	aag Lys	aaa Lys	ctg Leu	tgg Trp 580	gag Glu	caa Gln	acc Thr	cat His	tcc Ser 585	aaa Lys	gct Ala	gga Gly	ctg Leu	1957
ctg Leu 590	gtc Val	tcc Ser	gac Asp	gga Gly	ggc Gly 595	cca Pro	aat Asn	tta Leu	tac Tyr	aac Asn 600	att Ile	aga Arg	aat Asn	ctc Leu	cac His 605	2005
att Ile	cct Pro	gaa Glu	gtc Val	tgc Cys 610	ttg Leu	aaa Lys	tgg Trp	gaa Glu	tta Leu 615	atg Met	gat Asp	gag Glu	gat Asp	tac Tyr 620	cag Gln	2053
ggg Gly	cgt Arg	tta Leu	tgc Cys 625	aac Asn	cca Pro	ctg Leu	aac Asn	cca Pro 630	ttt Phe	gtc Val	aac Asn	cat His	aaa Lys 635	gac Asp	att Ile	2101
gaa Glu	tca Ser	gtg Val 640	aac Asn	aat Asn	gca Ala	gtg Val	ata Ile 645	atg Met	cca Pro	gca Ala	cat His	ggg Gly 650	cca Pro	gcc Ala	aaa Lys	2149
aac Asn 655	atg Met	gag Glu	tat Tyr	gat Asp	gct Ala	gtt Val 660	gca Ala	aca Thr	aca Thr	cac His	tcc Ser 665	tgg Trp	atc Ile	ccc Pro	aaa Lys	2197
aga Arg 670	aat Asn	cga Arg	tcc Ser	atc Ile	ttg Leu 675	aat Asn	aca Thr	agc Ser	caa Gln	aga Arg 680	gga Gly	ata Ile	ctt Leu	gaa Glu	gat Asp 685	2245
gaa Glu	caa Gln	atg Met	tac Tyr	caa Gln 690	aag Lys	tgc Cys	tgc Cys	aac Asn	tta Leu 695	ttt Phe	gaa Glu	aaa Lys	ttc Phe	ttc Phe 700	ccc Pro	2293
agc Ser	agt Ser	tca Ser	tac Tyr 705	aga Arg	aga Arg	cca Pro	gtc Val	ggg Gly 710	ata Ile	tcc Ser	agt Ser	atg Met	gtg Val 715	gag Glu	gct Ala	2341

atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730
 agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745
 att gaa gag ctg aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755
 atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctcccccg ggccgggagg tcgcgtcacc gaccacccg ccggcccagg cgacgcgcga 2611
 cacggacacc tgtcccaaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671
 tctggtcaac ccaggacac acgcgggagc agcgccggc cggggacgcc ctccggccg 2731
 cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa ccgacagga 3091
 ctataaagat accaggcgtt tccccctgga agctccctcg tgcgctctcc tgttccgacc 3151
 ctgccgetta ccgatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcgggt taggtcgttc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtc 3331
 aaccgcgtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcggtgc tacagagttc ttgaagtggc ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
 tctgacgctc agtgaacga aaactcacgt taagggaatt tggatcatgag attatcaaaa 3691
 aggatcttca cctagatcct tttaaattaa aaatgaagtc ttaaataat ctaaagtata 3751
 tatgagtaaa cttggtctga cagttaccaa tgcttaata gtgaggcacc tatctcagcg 3811
 atctgtctat ttggttcac catagttgcc tgactccccg tcgtgtagat aactacgata 3871
 cgggaggggt taccatctgg cccagtgct gcaatgacac cgcgagaccc acgctcaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgag aagtggctct 3991
 gcaactttat ccgcctccat ccagtctatt aattgttgcc ggaagctag agtaagtagt 4051
 tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc ggttcccaac gatcaaggcg agttacatga 4171

100737-000000
 200300-000000

```

<210> 39
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3246

<400> 39
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
  1             5             10             15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
          20             25             30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
      35             40             45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
  50             55             60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
  65             70             75             80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
          85             90             95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
      100             105             110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
      115             120             125

```

Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Thr	Ala	Leu	Ala	
130							135			140					
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser
145					150					155					160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys
				165					170					175	
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
			180					185					190		
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
		195					200					205			
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
	210					215					220				
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
225					230					235					240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
				245					250					255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro
			260					265					270		
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys
		275					280					285			
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	Ser	Phe	Thr	Ile	Thr	Gly
	290					295					300				
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala
305					310					315					320
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val
				325					330					335	
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly
			340					345					350		
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Leu	Arg	Thr	Gln	Ile
		355					360					365			
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Asp	Ser
	370					375					380				
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ile	Asp	Gly	Thr
385					390					395					400
Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	Met	Leu	Ser
				405					410					415	
Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	Gly	Gln	Lys	Arg	His	Thr
			420					425					430		
Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	Asp	Phe	Ala
		435					440					445			
Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	Gly	Val	Asn
	450					455					460				
Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Leu	Gly	Ile	Asn	Met	Ser	Lys	Lys
465					470						475				480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 40
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3247

<220>
 <221> CDS
 <222> (191)..(2461)

<400> 40

```

cccaaaaaaa aaaaaaaaaa aagagtccag agtggccccg ccgctccgcg ccgggggggg 60
gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
      Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
        1              5              10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
      15              20              25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
      30              35              40              45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
              50              55              60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
              65              70              75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
              80              85              90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
              95              100              105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
      110              115              120              125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
              130              135              140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
              145              150              155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
              160              165              170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
              175              180              185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
      190              195              200              205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
              210              215              220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
              225              230              235

```

1007337.000000

cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg	ggg Gly 250	ttt Phe	gta Val	tac Tyr	949
ttt Phe	gtt Val 255	gag Glu	aca Thr	cta Leu	gca Ala	agg Arg 260	agt Ser	ata Ile	tgt Cys	gag Glu	aaa Lys 265	ctt Leu	gaa Glu	caa Gln	tca Ser	997
gga Gly 270	ttg Leu	cca Pro	gtt Val	gga Gly	ggc Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gca Ala 280	aag Lys	ttg Leu	gca Ala	aat Asn	gtt Val 285	1045
gta Val	agg Arg	aag Lys	atg Met	atg Met 290	acc Thr	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
atc Ile	act Thr	gga Gly	gat Asp 305	aac Asn	acc Thr	aaa Lys	tgg Trp	aac Asn	gaa Glu	aat Asn	cag Gln	aac Asn	cct Pro 315	cgg Arg	atg Met	1141
ttt Phe	ttg Leu	gcc Ala 320	atg Met	atc Ile	aca Thr	tat Tyr	ata Ile 325	acc Thr	aga Arg	aat Asn	cag Gln	ccc Pro 330	gaa Glu	tgg Trp	ttc Phe	1189
aga Arg	aat Asn 335	gtt Val	cta Leu	agt Ser	att Ile	gct Ala 340	cca Pro	ata Ile	atg Met	ttc Phe	tca Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237
aga Arg 350	ctg Leu	gga Gly	aag Lys	ggg Gly	tac Tyr 355	atg Met	ttt Phe	gag Glu	agc Ser	aag Lys 360	agt Ser	atg Met	aaa Lys	att Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	cct Pro	gca Ala 370	gaa Glu	atg Met	cta Leu	gca Ala	agt Ser 375	att Ile	gat Asp	cta Leu	aaa Lys	tat Tyr 380	ttc Phe	1333
aat Asn	gaa Glu	cca Pro	aca Thr 385	agg Arg	aag Lys	aaa Lys	atc Ile	gag Glu 390	aaa Lys	ata Ile	agg Arg	cct Pro	ctc Leu 395	ata Ile	ata Ile	1381
gac Asp	ggc Gly	aca Thr 400	gcc Ala	tca Ser	tta Leu	agc Ser	cgc Pro 405	gga Gly	atg Met	atg Met	atg Met	ggt Gly 410	atg Met	ttc Phe	aac Asn	1429
atg Met	ctg Leu 415	agt Ser	aca Thr	gtg Val	ttg Leu	gga Gly 420	gtc Val	tca Ser	atc Ile	ctg Leu	aat Asn 425	ctt Leu	ggg Gly	caa Gln	aag Lys	1477
aga Arg 430	tac Tyr	acc Thr	aaa Lys	acc Thr	aca Thr 435	tac Tyr	tgg Trp	tgg Trp	gat Asp	gga Gly 440	ctt Leu	cag Gln	tcc Ser	tct Ser	gat Asp 445	1525
gat Asp	ttt Phe	gct Ala	ctc Leu	atc Ile 450	gtg Val	aat Asn	gca Ala	cca Pro	aat Asn 455	cat His	gag Glu	gga Gly	ata Ile	caa Gln 460	gcg Ala	1573
gga Gly	gtg Val	gat Asp	aga Arg 465	ttc Phe	tac Tyr	aga Arg	acc Thr	tgc Cys 470	aag Lys	cta Leu	gtt Val	ggg Gly	atc Ile 475	aat Asn	atg Met	1621
agc Ser	aag Lys	aaa Lys 480	aag Lys	tcc Ser	tat Tyr	ata Ile	aat Asn 485	agg Arg	aca Thr	gga Gly	aca Thr	ttc Phe 490	gaa Glu	ttc Phe	aca Thr	1669

agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu
 495 500 505

ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
 510 515 520 525

gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
 Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
 625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
 640 645 650

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2197
 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715

atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgctcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

20200207 14:00:00

atgccttgtt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611
 cagggacacc tgtccccaaa aacgrcacca tcgcagccac acacggagcg cccggggccc 2671
 tcttgtcaac ccagggacac acgcggggagc agcgccgggc cggggacgcc ctcccgggcg 2731
 cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cggggccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacaa aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091
 ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttccgacc 3151
 ctgccgctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcgggt taggtcgttc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331
 aaccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcgggtg tacagagttc ttgaagtggg ggccctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631
 tctgacgctc agtggaacga aaactcacgt taagggattt tggatcatgag attatcaaaa 3691
 aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataat ctaaagtata 3751
 tatgagtaaa cttgggtctga cagttaccaa tgcttaatca gtgaggcacc tatctcagcg 3811
 atctgtctat ttcgttcac ctagttgcc tgactccccg tcgtgtagat aactacgata 3871
 cgggagggct taccatctgg cccagtgct gcaatgatac cgcgagacct acgctcaccg 3931
 gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgag aagtggctct 3991
 gcaactttat ccgcctccat ccagtctatt aattgttgcc gggaagctag agtaagtagt 4051
 tcgccagtta atagtttgcg caacgttggt gccattgcta caggcatcgt ggtgtcacgc 4111
 tcgtcgtttg gtatggcttc attcagctcc ggttcccaac gatcaaggcg agttacatga 4171
 tccccatgt tgtgcaaaaa agcggttagc tccttcggtc ctccgatcgt tgtcagaagt 4231
 aagttggccg cagtgttacc actcatggtt atggcagcac tgcataattc tcttacgtc 4291
 atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa 4351
 tagtgtatgc ggcgaccgag ttgctcttgc ccggcgtaaa cacgggataa taccgcgcca 4411
 catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca 4471

aggatcttac cgctgttgag atccagttcg atgtaacca ctcgtgcacc caactgatct 4531
 tcagcatctt ttactttcac cagcgtttct gggtagagcaa aaacaggaag gcaaaatgcc 4591
 gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt cctttttcaa 4651
 tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt 4711
 tagaaaaata aacaaaagag tttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771
 ctgcttaatt tgatgcctgg cagtttatgg cgggcgtcct gcccgccacc ctccggggcg 4831
 ttgcttcgca acgttcaa at cgcctcccg cggtttgtc ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
 atgcctggca gttccctact ctgcgcatgg gagacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgccaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgattta at ctgtatcagg ctgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctagc ggccgac 5169

<210> 41
 <211> 757
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: pHL3247

<400> 41
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
 1 5 10 15
 Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
 20 25 30
 Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45
 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg	
		195					200					205				
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu	
	210					215					220					
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala	
225					230					235					240	
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu	
				245					250					255		
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro	
			260					265					270			
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys	
		275					280					285				
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly	
	290					295					300					
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala	
305					310					315					320	
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val	
				325					330					335		
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly	
			340					345					350			
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	Thr	Gln	Ile	
		355					360					365				
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Glu	Pro	
	370					375					380					
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Ile	Ile	Asp	Gly	Thr	
385					390					395					400	
Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	Met	Leu	Ser	
				405					410					415		
Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	Gly	Gln	Lys	Arg	Tyr	Thr	
			420					425					430			
Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	Asp	Phe	Ala	
		435					440					445				
Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	Gly	Val	Asp	
	450					455					460					
Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Val	Gly	Ile	Asn	Met	Ser	Lys	Lys	
465					470					475					480	
Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	Phe	Glu	Phe	Thr	Ser	Phe	Phe	
				485					490					495		
Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	Met	Glu	Leu	Pro	Ser	Phe	
			500				505						510			
Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	Met	Ser	Ile	Gly	Val	Thr	
		515					520					525				
Val	Ile	Lys	Asn	Asn	Met	Ile	Asn</									

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 42
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3258

<220>
 <221> CDS
 <222> (191)..(2461)

<400> 42
 cccaaaaaaa aaaaaaaaaa aagagtccag agtggccccg ccgctccgcg ccggggggggg 60
 gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
 acaaagtgtc gcccgaggta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

200020-222200

gca Ala	caa Gln 15	aat Asn	gct Ala	ata Ile	agc Ser	aca Thr 20	act Thr	ttc Phe	cct Pro	tat Tyr	act Thr 25	gga Gly	gac Asp	cct Pro	cct Pro	277
tac Tyr 30	agc Ser	cat His	ggg Gly	aca Thr	gga Gly 35	aca Thr	gga Gly	tac Tyr	acc Thr	atg Met 40	gat Asp	act Thr	gtc Val	aac Asn	agg Arg 45	325
aca Thr	cat His	cag Gln	tac Tyr	tca Ser 50	gaa Glu	agg Arg	gga Gly	aga Arg	tgg Trp 55	aca Thr	aca Thr	aac Asn	acc Thr	gaa Glu 60	act Thr	373
gga Gly	gca Ala	ccg Pro	caa Gln 65	ctc Leu	aac Asn	ccg Pro	att Ile	gat Asp 70	ggg Gly	cca Pro	ctg Leu	cca Pro	gaa Glu 75	gac Asp	aat Asn	421
gaa Glu	cca Pro	agt Ser 80	ggt Gly	tat Tyr	gcc Ala	caa Gln	aca Thr 85	gat Asp	tgt Cys	gta Val	ttg Leu 90	gaa Glu 90	gca Ala	atg Met	gcc Ala	469
ttc Phe 95	ctt Leu	gag Glu	gaa Glu	tcc Ser	cat His	cct Pro 100	ggt Gly	atc Ile	ttt Phe	gag Glu	acc Thr 105	tcg Ser	tgt Cys	ctt Leu	gaa Glu	517
acg Thr 110	atg Met	gag Glu	gtt Val	gtt Val	cag Gln 115	caa Gln	aca Thr	cga Arg	gtg Val	gac Asp 120	aag Lys	ctg Leu	aca Thr	caa Gln	ggc Gly 125	565
cga Arg	cag Gln	acc Thr	tat Tyr	gac Asp 130	tgg Trp	act Thr	cta Leu	aat Asn	agg Arg 135	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	aca Thr	613
gca Ala	ttg Leu	gcc Ala	aac Asn 145	aca Thr	ata Ile	gaa Glu	gtg Val	ttc Phe 150	aga Arg	tca Ser	aat Asn	ggc Gly	ctc Leu 155	acg Thr	gcc Ala	661
aat Asn	gaa Glu	tct Ser 160	gga Gly	agg Arg	ctc Leu	ata Ile	gac Asp 165	ttc Phe	ctt Leu	aag Lys	gat Asp	gta Val 170	atg Met	gag Glu	tca Ser	709
atg Met	aac Asn 175	aaa Lys	gaa Glu	gaa Glu	atg Met	gag Glu 180	atc Ile	aca Thr	act Thr	cat His	ttt Phe 185	cag Gln	aga Arg	aag Lys	aga Arg	757
cga Arg 190	gtg Val	aga Arg	gac Asp	aat Asn	atg Met 195	act Thr	aag Lys	aaa Lys	atg Met	gtg Val 200	aca Thr	cag Gln	aga Arg	aca Thr	ata Ile 205	805
ggt Gly	aaa Lys	agg Arg	aag Lys	cag Gln 210	aga Arg	ttg Leu	aac Asn	aaa Lys	agg Arg 215	agt Ser	tat Tyr	cta Leu	att Ile	agg Arg 220	gca Ala	853
tta Leu	acc Thr	ctg Leu	aac Asn 225	aca Thr	atg Met	acc Thr	aaa Lys	gat Asp 230	gct Ala	gag Glu	aga Arg	ggg Gly	aag Lys 235	cta Leu	aaa Lys	901
cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg	ggg Gly 250	ttt Phe	gta Val	tac Tyr	949
ttt Phe 255	gtt Val	gag Glu	aca Thr	cta Leu	gca Ala	agg Arg 260	agt Ser	ata Ile	tgt Cys	gag Glu	aaa Lys 265	ctt Leu	gaa Glu	caa Gln	tca Ser	997
gga Gly 270	ttg Leu	cca Pro	gtt Val	gga Gly 275	ggc Asn	aat Asn	gag Glu	aag Lys	aaa Lys	gca Ala 280	aag Lys	ttg Leu	gca Ala	aat Asn	gtt Val 285	1045

gta Val	agg Arg	aag Lys	atg Met	atg Met 290	acc Thr	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
atc Ile	act Thr	gga Gly	gat Asp 305	aac Asn	acc Thr	aaa Lys	tgg Trp	aac Asn 310	gaa Glu	aat Asn	cag Gln	aac Asn	cct Pro 315	cgg Arg	atg Met	1141
ttt Phe	ttg Leu	gcc Ala 320	atg Met	atc Ile	aca Thr	tat Tyr	ata Ile 325	acc Thr	aga Arg	aat Asn	cag Gln	ccc Pro 330	gaa Glu	tgg Trp	ttc Phe	1189
aga Arg	aat Asn 335	gtt Val	cta Leu	agt Ser	att Ile	gct Ala 340	cca Pro	ata Ile	atg Met	ttc Phe	tca Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237
aga Arg 350	ctg Leu	gga Gly	aag Lys	ggg Gly 355	tac Tyr	atg Met	ttt Phe	gag Glu	agc Ser	aag Lys 360	agt Ser	atg Met	aaa Lys	att Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	cct Pro	gca Ala 370	gaa Glu	atg Met	cta Leu	gca Ala	agt Ser 375	att Ile	gat Asp	cta Leu	aaa Lys	tat Tyr 380	ttc Phe	1333
aat Asn	gaa Glu	cca Pro	aca Thr 385	agg Arg	aag Lys	aaa Lys	atc Ile	gag Glu 390	aaa Lys	ata Ile	agg Arg	cct Pro	ctc Leu 395	tta Leu	ata Ile	1381
gat Asp	ggg Gly	act Thr 400	gca Ala	tca Ser	ttg Leu	agc Ser	cct Pro 405	gga Gly	atg Met	atg Met	atg Met	ggc Gly 410	atg Met	ttc Phe	aat Asn	1429
atg Met	tta Leu 415	agt Ser	act Thr	gta Val	tta Leu	ggc Gly 420	gtc Val	tcc Ser	atc Ile	ctg Leu	aat Asn 425	ctt Leu	gga Gly	caa Gln	aag Lys	1477
aga Arg 430	cac His	acc Thr	aag Lys	act Thr	act Thr 435	tac Tyr	tgg Trp	tgg Trp	gat Asp	ggg Gly 440	ctt Leu	caa Gln	tct Ser	tct Ser	gat Asp 445	1525
gat Asp	ttt Phe	gct Ala	ctg Leu	att Ile 450	gtg Val	aat Asn	gca Ala	ccc Pro	aat Asn 455	cat His	gaa Glu	ggg Gly	att Ile	caa Gln 460	gcc Ala	1573
gga Gly	gtc Val	aac Asn	agg Arg 465	ttt Phe	tat Tyr	cga Arg	acc Thr	tgt Cys 470	aag Lys	cta Leu	ctt Leu	gga Gly	att Ile 475	aat Asn	atg Met	1621
agc Ser	aag Lys	aaa Lys 480	aag Lys	tct Ser	tac Tyr	ata Ile	aac Asn 485	aga Arg	aca Thr	ggg Gly	aca Thr	ttt Phe 490	gaa Glu	ttc Phe	aca Thr	1669
agc Ser	ttt Phe 495	ttc Phe	tat Tyr	cgt Arg	tat Tyr	ggg Gly 500	ttt Phe	gtt Val	gcc Ala	aat Asn	ttc Phe 505	agc Ser	atg Met	gag Glu	ctt Leu	1717
ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggg Gly 540	cca Pro	1813
gca	acc	gct	caa	atg	gcc	ctt	cag	ctg	ttc	atc	aaa	gat	tac	agg	tac	1861

[illegible]

cggg	ccgcac	gogcgcctcag	ggagcgcctct	ccgactccgc	acggggactc	gccagaaaagg	2911
atcgt	gacct	gcattaatga	atcaggggat	aacgcaggaa	agaacatgtg	agcaaaaggc	2971
cagcaaaaagg	ccaggaaccg	taaaaaggcc	gcgttgctgg	cgtttttcca	taggctccgc		3031
ccccctgacg	agcatcacaa	aatcgacgc	tcaagtcaga	ggtggcgaaa	ccgcacagga		3091
ctataaagat	accaggcggt	tccccctgga	agctccctcg	tgcgctctcc	tgttccgacc		3151
ctgccgctta	ccggatacct	gtccgccttt	ctcccttcgg	gaagcgtggc	gctttctcat		3211
agctcacgct	gtaggatatct	cagttcggtg	taggtcgttc	gctccaagct	gggctgtgtg		3271
cacgaacccc	ccgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tottgagtcc		3331
aacccggtaa	gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gattagcaga		3391
gcgaggtatg	taggcgggtgc	tacagagttc	ttgaagtgg	ggcctaacta	cggctacact		3451
agaaggacag	tatttggtat	ctgcgctctg	ctgaagccag	ttaccttcgg	aaaaagagtt		3511
ggtagctctt	gatccggcaa	acaaaccacc	gctggtagcg	gtggtttttt	tgtttgcaag		3571
cagcagatta	cgcgcagaaa	aaaaggatct	caagaagatc	ctttgatctt	ttctacgggg		3631
tctgacgctc	agtggaacga	aaactcacgt	taagggattt	tggtcatgag	attatcaaaa		3691
aggatcttca	cctagatcct	tttaaattaa	aatgaagtt	ttaaataaat	ctaaagtata		3751
tatgagtaaa	cttgggtctga	cagttaccaa	tgcttaatca	gtgaggcacc	tatctcagcg		3811
atctgtctat	ttcgttcctc	catagttgcc	tgactccccg	tcgtgtagat	aactacgata		3871
cgggagggct	taccatctgg	cccagtgct	gcaatgatac	cgcgagaccc	acgctcaccg		3931
gctccagatt	tatcagcaat	aaaccagcca	gccggaagg	ccgagcgcag	aagtggctct		3991
gcaactttat	ccgcctccat	ccagtctatt	aattgttgcc	gggaagctag	agtaagtagt		4051
tcgccagtta	atagtttgcg	caacgttggt	gccattgcta	caggcatcgt	ggtgtcacgc		4111
tcgtcgtttg	gtatggcttc	attcagctcc	ggttcccaac	gatcaaggcg	agttacatga		4171
tcccccatgt	tgtgcaaaaa	agcggttagc	tccttcggtc	ctccgatcgt	tgtcagaagt		4231
aagttggccg	cagtgttata	actcatgggt	atggcagcac	tgcataattc	tcttactgtc		4291
atgccatccg	taagatgctt	ttctgtgact	ggtgagtact	caaccaagtc	attctgagaa		4351
tagtgatatgc	ggcgaccgag	ttgctcttgc	ccggcgtcaa	cacgggataa	taccgcgcca		4411
catagcagaa	ctttaaaagt	gctcatcatt	ggaaaacgtt	cttcggggcg	aaaactctca		4471
aggatcttac	cgctgttgag	atccagttcg	atgtaacca	ctcgtgcacc	caactgatct		4531
tcagcatctt	ttactttcac	cagcgtttct	gggtgagcaa	aaacaggaag	gcaaaatgcc		4591
gcaaaaaagg	gaataagggc	gacacggaaa	tggtgaatac	tcataactct	cctttttcaa		4651
tattattgaa	gcatttatca	gggttattgt	ctcatgagcg	gatacatatt	tgaatgtatt		4711
tagaaaaata	aacaaaagag	tttgtagaaa	cgcaaaaagg	ccatccgtca	ggatggcctt		4771
ctgcttaatt	tgatgcctgg	cagtttatgg	cgggcgtcct	gcccgccacc	ctccggggcg		4831
ttgcttcgca	acgttcaaat	ccgctcccg	cggatttgct	ctactcagga	gagcgttcac		4891

```
<210> 43
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3258
```

<400>	43															
Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro	Ala	Gln	Asn	
1				5					10					15		
Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	Tyr	Ser	His	
			20					25					30			
Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln	
		35					40					45				
Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro	
	50					55					60					
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser	
65					70					75					80	
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu	
				85					90					95		
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu	
			100					105					110			
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr	
		115					120					125				
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala	
	130					135					140					
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser	
145					150					155					160	
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys	
				165					170					175		
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg	
			180					185					190			
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg	
		195					200					205				
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu	
	210					215					220					
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala	
225					230					235					240	
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu	
				245					250					255		

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605

20250220 14:22:00

```
<210> 44
<211> 5169
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> CDS  
<222> (191)..(2461)
```

```

<400> 44
ccccaaaaaaaa aaaaaaaaaa aagagtccag agtggccccc cgcgtccgcg ccgggggggg 60
gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120
acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca      229
      Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
          1              5                  10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct      277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
      15              20                  25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg      325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
      30              35                  40                  45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act      373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
          50              55                  60

```

gga Gly	gca Ala	ccg Pro	caa Gln 65	ctc Leu	aac Asn	ccg Pro	att Ile	gat Asp 70	ggg Gly	cca Pro	ctg Leu	cca Pro	gaa Glu 75	gac Asp	aat Asn	421
gaa Glu	cca Pro	agt Ser 80	ggt Gly	tat Tyr	gcc Ala	caa Gln	aca Thr 85	gat Asp	tgt Cys	gta Val	ttg Leu 90	gaa Glu 90	gca Ala	atg Met	gcc Ala	469
ttc Phe	ctt Leu 95	gag Glu	gaa Glu	tcc Ser	cat His	cct Pro 100	ggt Gly	atc Ile	ttt Phe	gag Glu	acc Thr 105	tcg Ser	tgt Cys	ctt Leu	gaa Glu	517
acg Thr 110	atg Met	gag Glu	gtt Val	gtt Val	cag Gln 115	caa Gln	aca Thr	cga Arg	gtg Val	gac Asp 120	aag Lys	ctg Leu	aca Thr	caa Gln	ggc Gly 125	565
cga Arg	cag Gln	acc Thr	tat Tyr	gac Asp 130	tgg Trp	act Thr	cta Leu	aat Asn	agg Arg 135	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	aca Thr	613
gca Ala	ttg Leu	gcc Ala	aac Asn 145	aca Thr	ata Ile	gaa Glu	gtg Val	ttc Phe 150	aga Arg	tca Ser	aat Asn	ggc Gly 155	ctc Leu 155	acg Thr	gcc Ala	661
aat Asn	gaa Glu	tct Ser 160	gga Gly	agg Arg	ctc Leu	ata Ile	gac Asp 165	ttc Phe	ctt Leu	aag Lys	gat Asp 170	gta Val	atg Met	gag Glu	tca Ser	709
atg Met	aac Asn 175	aaa Lys	gaa Glu	gaa Glu	atg Met	gag Glu 180	atc Ile	aca Thr	act Thr	cat His	ttt Phe 185	cag Gln	aga Arg	aag Lys	aga Arg	757
cga Arg 190	gtg Val	aga Arg	gac Asp	aat Asn	atg Met 195	act Thr	aag Lys	aaa Lys	atg Met	gtg Val 200	aca Thr	cag Gln	aga Arg	aca Thr	ata Ile 205	805
ggt Gly	aaa Lys	agg Arg	aag Lys	cag Gln 210	aga Arg	ttg Leu	aac Asn	aaa Lys	agg Arg 215	agt Ser	tat Tyr	cta Leu	att Ile	agg Arg 220	gca Ala	853
tta Leu	acc Thr	ctg Leu	aac Asn 225	aca Thr	atg Met	acc Thr	aaa Lys	gat Asp 230	gct Ala	gag Glu	aga Arg	ggg Gly 235	aag Lys	cta Leu	aaa Lys	901
cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg	ggg Gly 250	ttt Phe	gta Val	tac Tyr	949
ttt Phe	gtt Val 255	gag Glu	aca Thr	cta Leu	gca Ala	agg Arg 260	agt Ser	ata Ile	tgt Cys	gag Glu	aaa Lys 265	ctt Leu	gaa Glu	caa Gln	tca Ser	997
gga Gly 270	ttg Leu	cca Pro	gtt Val	gga Gly	ggc Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gca Ala 280	aag Lys	ttg Leu	gca Ala	aat Asn	gtt Val 285	1045
gta Val	agg Arg	aag Lys	atg Met	atg Met	acc Thr 290	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
atc Ile	act Thr	gga Gly 305	gat Asp	aac Asn	acc Thr	aaa Lys	tgg Trp	aac Asn 310	gaa Glu	aat Asn	cag Gln	aac Asn	cct Pro 315	cgg Arg	atg Met	1141
ttt Phe	ttg Leu	gcc Ala 320	atg Met	atc Ile	aca Thr	tat Tyr 325	ata Ile	acc Thr	aga Arg	aat Asn	cag Gln	ccc Pro 330	gaa Glu	tgg Trp	ttc Phe	1189

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
 350 355 360 365

act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc tta ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile
 385 390 395

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat 1525
 Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg 1621
 Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met
 465 470 475

agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu
 495 500 505

ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
 510 515 520 525

gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu
 575 580 585

19930722E2001

ttg gtt tca gat ggc gga cca aac ctg tac aac att cga aat ctc cac Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 590 595 600 605	2005
att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile 625 630 635	2101
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys 640 645 650	2149
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys 655 660 665	2197
aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp 670 675 680 685	2245
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Phe Glu Lys Phe Pro 690 695 700	2293
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala 705 710 715	2341
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly 720 725 730	2389
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr 735 740 745	2437
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgctct tcatgaaaa Ile Glu Glu Leu Arg Arg Gln Lys 750 755	2491
atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata	2551
cctcccccg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga	2611
cacggacacc tgtcccaaaa aacgccacca tcgcagccac acacggagcg ccggyggccc	2671
tctggtcaac ccaggacac acgcgggagc agcgccgggc cggggacgcc ctcccgcccg	2731
cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg	2791
gccggcccct cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct	2851
cgggcccgcac gcgcgctcag ggagcgctct ccgactccgc acggggactc gccagaaagg	2911
atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc	2971
cagcaaaagg ccaggaaccg taataaaggcc gcgttgcttg cgttttttcca taggctccgc	3031
ccccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga	3091
ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttccgacc	3151
ctgcgcctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat	3211

5169

<400>	45														
Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro	Ala	Gln	Asn
1				5					10					15	
Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	Tyr	Ser	His
			20					25					30		
Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln
		35					40					45			
Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
	50					55					60				
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser
65					70					75					80
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu
				85					90					95	
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu
			100					105					110		
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
		115					120					125			
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala
	130					135					140				
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser
145					150					155					160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys
				165					170					175	
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
			180					185					190		
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
		195					200					205			
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
	210					215					220				
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
225					230					235					240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
				245					250					255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro
			260					265					270		
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys
		275					280					285			
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly
	290					295					300				
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala
305					310					315					320

Met	Ile	Thr	Tyr	Ile 325	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335	Val
Leu	Ser	Ile	Ala 340	Pro	Ile	Met	Phe	Ser 345	Asn	Lys	Met	Ala	Arg 350	Leu	Gly
Lys	Gly	Tyr	Met 355	Phe	Glu	Ser	Lys 360	Ser	Met	Lys	Ile	Arg 365	Thr	Gln	Ile
Pro	Ala 370	Glu	Met	Leu	Ala	Ser 375	Ile	Asp	Leu	Lys	Tyr 380	Phe	Asn	Glu	Pro
Thr 385	Arg	Lys	Lys	Ile	Glu 390	Lys	Ile	Arg	Pro	Leu 395	Leu	Ile	Asp	Gly	Thr 400
Ala	Ser	Leu	Ser	Pro 405	Gly	Met	Met	Met	Gly 410	Met	Phe	Asn	Met	Leu 415	Ser
Thr	Val	Leu	Gly 420	Val	Ser	Ile	Leu	Asn 425	Leu	Gly	Gln	Lys	Arg 430	His	Thr
Lys	Thr	Thr 435	Tyr	Trp	Trp	Asp	Gly 440	Leu	Gln	Ser	Ser	Asp 445	Asp	Phe	Ala
Leu	Ile 450	Val	Asn	Ala	Pro	Asn 455	His	Glu	Gly	Ile	Gln 460	Ala	Gly	Val	Asn
Arg 465	Phe	Tyr	Arg	Thr	Cys 470	Lys	Leu	Leu	Gly	Ile 475	Asn	Met	Ser	Lys	Lys 480
Lys	Ser	Tyr	Ile	Asn 485	Arg	Thr	Gly	Thr	Phe 490	Glu	Phe	Thr	Ser	Phe 495	Phe
Tyr	Arg	Tyr	Gly 500	Phe	Val	Ala	Asn	Phe 505	Ser	Met	Glu	Leu	Pro 510	Ser	Phe
Gly	Val	Ser 515	Gly	Ile	Asn	Glu	Ser 520	Ala	Asp	Met	Ser	Ile 525	Gly	Val	Thr
Val	Ile 530	Lys	Asn	Asn	Met	Ile 535	Asn	Asn	Asp	Leu	Gly 540	Pro	Ala	Thr	Ala
Gln 545	Met	Ala	Leu	Gln	Leu 550	Phe	Ile	Lys	Asp	Tyr 555	Arg	Tyr	Thr	Tyr	Arg 560
Cys	His	Arg	Gly	Asp 565	Thr	Gln	Ile	Gln	Thr 570	Arg	Arg	Ser	Phe	Glu 575	Leu
Lys	Lys	Leu 580	Trp	Glu	Gln	Thr	Arg	Ser 585	Lys	Ala	Gly	Leu	Leu 590	Val	Ser
Asp	Gly	Gly 595	Pro	Asn	Leu	Tyr	Asn 600	Ile	Arg	Asn	Leu	His 605	Ile	Pro	Glu
Val	Cys 610	Leu	Lys	Trp	Glu	Leu 615	Met	Asp	Glu	Asp	Tyr 620	Gln	Gly	Arg	Leu
Cys 625	Asn	Pro	Leu	Asn	Pro 630	Phe	Val	Asn	His	Lys 635	Asp	Ile	Glu	Ser	Val 640
Asn	Asn	Ala	Val	Ile 645	Met	Pro	Ala	His	Gly 650	Pro	Ala	Lys	Asn	Met 655	Glu
Tyr	Asp	Ala 660	Val	Ala	Thr	Thr	His 665	Ser	Trp	Ile	Pro	Lys	Arg 670	Asn	Arg

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

<210> 46

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3268

<220>

<221> CDS

<222> (191)..(2461)

<400> 46

ccccaaaaaa aaaaaaaaaa aagagtccag agtggccccc cgcgtccgcg ccgggggggg 60

gggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaaa 120

acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565

10073377.0208002

Thr 110	Met	Glu	Val	Val	Gln 115	Gln	Thr	Arg	Val	Asp 120	Lys	Leu	Thr	Gln	Gly 125	
cga Arg	cag Gln	acc Thr	tat Tyr	gac Asp 130	tgg Trp	act Thr	cta Leu	aat Asn	agg Arg 135	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	aca Thr	613
gca Ala	ttg Leu	gcc Ala	aac Asn 145	aca Thr	ata Ile	gaa Glu	gtg Val	ttc Phe 150	aga Arg	tca Ser	aat Asn	ggc Gly 155	ctc Leu	acg Thr	gcc Ala	661
aat Asn	gaa Glu	tct Ser 160	gga Gly	agg Arg	ctc Leu	ata Ile	gac Asp 165	ttc Phe	ctt Leu	aag Lys	gat Asp 170	gta Val	atg Met	gag Glu	tca Ser	709
atg Met 175	aac Asn	aaa Lys	gaa Glu	gaa Glu	atg Met	gag Glu	atc Ile	aca Thr	act Thr	cat His	ttt Phe 185	cag Gln	aga Arg	aag Lys	aga Arg	757
cga Arg 190	gtg Val	aga Arg	gac Asp	aat Asn	atg Met 195	act Thr	aag Lys	aaa Lys	atg Met 200	gtg Val	aca Thr	cag Gln	aga Arg	aca Thr	ata Ile 205	805
ggt Gly	aaa Lys	agg Arg	aag Lys	cag Gln 210	aga Arg	ttg Leu	aac Asn	aaa Lys	agg Arg 215	agt Ser	tat Tyr	cta Leu	att Ile	agg Arg 220	gca Ala	853
tta Leu	acc Thr	ctg Leu	aac Asn 225	aca Thr	atg Met	acc Thr	aaa Lys	gat Asp 230	gct Ala	gag Glu	aga Arg	ggg Gly	aag Lys 235	cta Leu	aaa Lys	901
cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg 250	ggg Gly	ttt Phe	gta Val	tac Tyr	949
ttt Phe 255	gtt Val	gag Glu	aca Thr	cta Leu	gca Ala	agg Arg 260	agt Ser	ata Ile	tgt Cys	gag Glu	aaa Lys 265	ctt Leu	gaa Glu	caa Gln	tca Ser	997
gga Gly 270	ttg Leu	cca Pro	gtt Val	gga Gly	ggc Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gca Ala 280	aag Lys	ttg Leu	gca Ala	aat Asn	gtt Val 285	1045
gta Val	agg Arg	aag Lys	atg Met	atg Met	acc Thr	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
atc Ile	act Thr	gga Gly	gat Asp 305	aac Asn	acc Thr	aaa Lys	tgg Trp	aac Asn	gaa Glu	aat Asn	cag Gln	aac Asn	cct Pro	cgg Arg	atg Met	1141
ttt Phe	ttg Leu	gcc Ala 320	atg Met	atc Ile	aca Thr	tat Tyr	ata Ile 325	acc Thr	aga Arg	aat Asn	cag Gln	ccc Pro	gaa Glu	tgg Trp	ttc Phe	1189
aga Arg	aat Asn 335	gtt Val	cta Leu	agt Ser	att Ile	gct Ala	cca Pro 340	ata Ile	atg Met	ttc Phe	tca Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237
aga Arg 350	ctg Leu	gga Gly	aag Lys	ggg Gly	tac Tyr 355	atg Met	ttt Phe	gag Glu	agc Ser	aag Lys 360	agt Ser	atg Met	aaa Lys	att Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	cct Pro	gca Ala 370	gaa Glu	atg Met	cta Leu	gca Ala	agt Ser 375	att Ile	gat Asp	cta Leu	aaa Lys	tat Tyr	ttc Phe 380	1333

10073377-00000000

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc tta ata	1381
Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile	
385 390 395	
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat	1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn	
400 405 410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag	1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat	1525
Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp	
430 435 440 445	
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc	1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg	1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca	1669
Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac	1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr	
545 550 555	
acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	
ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg	1957
Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu	
575 580 585	
ctg gtc tcc gac gga ggc cca aat tta tac aac att cgg aat ctc cac	2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His	
590 595 600 605	
atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag	2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln	
610 615 620	
gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att	2101
Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile	
625 630 635	
gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa	2149
Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys	
640 645 650	

10073377-0208002

agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag 2197
 Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665
 aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685
 gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700
 agc agc tca tac aga aga cca gtt gga att tcc agt atg gtg gag gcc 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715
 atg gtg tct agg gcc cgg att gat gca cga att gac ttc gag tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730
 agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745
 att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755
 atgccttggt tctactaata acccggcggc ccaaaatgcc gactcggagc gaaagatata 2551
 cctccccggg ggccgggagg tcgcgtcacc gaccacgccg ccggcccagg cgacgcgcga 2611
 cacggacacc tgtcccaaaa aacgccacca tcgcagccac acacggagcg cccggggccc 2671
 tctggtcaac ccaggacac acgcgggagc agcgccgggc cggggacgcc ctcccggccg 2731
 cccgtgccac acgcaggggg ccggcccgtg tctccagagc gggagccgga agcattttcg 2791
 gccggccctt cctacgaccg ggacacacga gggaccgaag gccggccagg cgcgacctct 2851
 cgggcccgcac gcgcgctcag ggagcgtctt ccgactccgc acggggactc gccagaaagg 2911
 atcgtgacct gcattaatga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc 2971
 cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc 3031
 cccctgacg agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga 3091
 ctataaagat accaggcggt tccccctgga agctccctcg tgcgctctcc tgttccgacc 3151
 ctgccgctta ccgataacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat 3211
 agctcacgct gtaggtatct cagttcggtg taggtcgttc gctccaagct gggctgtgtg 3271
 cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc 3331
 aaccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga 3391
 gcgaggtatg taggcgggtg tacagagttc ttgaagtggg ggcctaacta cggctacact 3451
 agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt 3511
 ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtgggttttt tgtttgcaag 3571
 cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg 3631

20220727 10:33:47

```
<210> 47
<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3268
```

```

<400> 47
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
  1             5             10             15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
             20             25             30

```

Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln	
		35					40					45				
Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro	
	50					55					60					
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser	
65					70					75					80	
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu	
				85					90					95		
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu	
			100					105					110			
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr	
		115					120					125				
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala	
	130					135					140					
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser	
145					150					155					160	
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys	
				165					170					175		
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg	
			180					185					190			
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg	
		195					200					205				
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu	
	210					215					220					
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala	
225					230					235					240	
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu	
				245					250					255		
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro	
			260					265					270			
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys	
		275					280					285				
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly	
	290					295					300					
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala	
305					310					315					320	
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val	
				325					330					335		
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly	
			340					345					350			
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	Thr	Gln	Ile	
		355					360					365				
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp								

Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

20220220 22:44:00

Leu Arg Arg Gln Lys
755

[illegible]